

QY 495 ESDLLKTLPTTQVLAALADVNFSSISKVDLFFKCDTOMITMDLRLKSVLYLPGDFVCK 554
DB 301 ESDLLKTLPTTQVLAALADVNFSSISKVDLFFKCDTOMITMDLRLKSVLYLPGDFVCK 360
QY 555 GEIGEMWYIKRGEVOVLGGPDGTAVLYLTKAGSVGEISLLAAGGNRTANVAVAHGA 614
DB 361 GEIGEMWYIKRGEVOVLGGPDGTAVLYLTKAGSV-----LLAAGGNRTANVAVAHGA 415
QY 615 NLTLTDKTLQELIIVHPDSEIRILMKKARVLLKOKAKTAATPPRKDLALLPPEKEETPK 674
DB 416 NLTLTDKTLQELIIVHPDSEIRILMKKARVLLKOKAKTAATPPRKDLALLPPEKEETPK 475
QY 675 LFKTLGGTGKASLARLLKKEQAAQKKENSEGEGEKKENEDKQKEDKQKEDKQ 734
DB 476 LFKTLGGTGKASLARLLKKEQAAQKKENSEGEGEKKENEDKQKEDKQKEDKQ 535
QY 735 KENEDKQKREBEKPEPLDREPECTASPIAVEEPHSVRVLRGRSROSLIISMAPSAG 794
DB 536 KENEDKQKREBEKPEPLDREPECTASPIAVEEPHSVRVLRGRSROSLIISMAPSAG 595
QY 795 GEEVLTIEVEKAKQ 809
DB 596 GEEVLTIEVEKAKQ 610

RESULT 2
US-09-949-016-11669
Sequence 11669, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11669
LENGTH: 416
TYPE: PRT
ORGANISM: Human
US-09-949-016-11669

Query Match 52.0%; Score 2202; DB 2; Length 416;
Best Local Similarity 99.8%; Pred. No. 1e-186; Mismatches 1; Indels 0; Gaps 0;
Matches 412; Conservative 0;

QY 114 POKKPPAAVINEYADAQHLNLYKRNRORTALYKKKLVEGDLSSEPSAPQAKPTAVPV 173
DB 1 POKKPPAAVINEYADAQHLNLYKRNRORTALYKKKLVEGDLSSEPSAPQAKPTAVPV 60
QY 174 KESDOKPTEHYRRLMFKYKMPLETKRIKLPNSIDYTDRLYLMLLTVLAVNNMC 233
DB 61 KESDOKPTEHYRRLMFKYKMPLETKRIKLPNSIDYTDRLYLMLLTVLAVNNMC 120
QY 234 WFLPLRVLPYQADNIHYMLADIICDIILYDMFLIOPRLOFVAGGDIIVDSNELRG 293
DB 121 WFLPLRVLPYQADNIHYMLADIICDIILYDMFLIOPRLOFVAGGDIIVDSNELRG 180
QY 294 YRTSTKFOLDVASIIPFDICYLLFGFNPMFRANRMLKYSFEEFNHLSIMDKAYIRV 353
DB 181 YRTSTKFOLDVASIIPFDICYLLFGFNPMFRANRMLKYSFEEFNHLSIMDKAYIRV 240
QY 354 INTTGYLFIHLINACVYVWASNYSGITTRWVYDGEENYLRQYVAVRLLITIGLPE 413
DB 241 INTTGYLFIHLINACVYVWASNYSGITTRWVYDGEENYLRQYVAVRLLITIGLPE 300

QY 414 PQLTFEIVFOLLNFPSSGVFVSSLLIGMRDVI GAATANQYFRACMDPTIAMNNYSIPK 473
DB 301 PQLTFEIVFOLLNFPSSGVFVSSLLIGMRDVI GAATANQYFRACMDPTIAMNNYSIPK 360
QY 474 LVOKRVRTWYETWDSQRMDESDLLKTLPTTQVLAALADVNFSSISKVDLFX 526
DB 361 LVOKRVRTWYETWDSQRMDESDLLKTLPTTQVLAALADVNFSSISKVDLFX 413

RESULT 3
US-09-538-092-1315
Sequence 1315, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapateSeqFormatter Version 0.9
SEQ ID NO 1315
LENGTH: 909
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)-(0)
OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

Query Match 46.0%; Score 1949; DB 2; Length 909;
Best Local Similarity 46.2%; Pred. No. 9.8e-164; Mismatches 238; Indels 110; Gaps 18;
Matches 403; Conservative 122;

QY 14 IGNNENQSSRRNEGSHPSNOSQTTAOE--ENKGE--EKSILKTSPTVTSSEPHTN 68
DB 67 VGEBAKKEAEKAEKAEAEVEEAEKEPODAETKEPEAEAEASGVPATKQHPVO 126
QY 69 IODK-----LSKNSSGDLTTNPDPQMAAEPRTVPEQKEMDGKGN----- 112
DB 127 VEDTDADSCPLMAEENPPS--TVLPSPAPASDTLIVPSASGTRHKKLPSEDDAEELK 184
QY 113 --SPONKP-----PAAP-----VINEYADAQHLNLYKRNRORTALY 146
DB 165 ALSPAESVYVWMSDDPTTKEDTDGODRASTASTNSAIIND----RLQELVTLFKERTBY 240
QY 147 KKLVEGDLS---SPEASPOQAKPTAVPVKESDCKPT--EHYRRLMFKYKMPLETKY 200
DB 241 KKLIDPVTSDSESPKSPAKKAPEDTPAPAEVVEEHHYCDMLCKFKHRPWKKY 300
QY 201 LKRITLPSIDYTPRRLYLMLLTVLAVNNMCWFLPLRVLPYQADNIHYMLADIIC 260
DB 301 ----OPSIDPLINLMLVLMFLFVVMAMNNMCWFLPLRVLPYQADNIHYMLADIIC 356
QY 261 DIILYDMFLIOPRLOFVAGGDIIVDSNELRGHYRTSTKFOLDVASIIPFDICYLLFGFN 320
DB 357 DIILYDMFLIOPRLOFVAGGDIITDKDMRNLYKSRFRKMDLSLPLDLYLKVGN 416
QY 321 PMFRANRMLKYSFEEFNHLSIMDKAYIRVIRTTGYLFIHLINACVYVWASNYSGI 380
DB 417 PLRLPRCLKMYAFEPFNSRLESILSKAYVVRITVAVLSTHNSCLYMAAYOGL 476
QY 381 GTTRWVYDGEENYLRQYVAVRLLITIGLPEPQTLFEIVFOLLNFPSSGVFVSSLLIG 440
DB 477 GSTHWVYDGEENYLRQYVAVRLLITIGLPEPQTLFEIVFOLLNFPSSGVFVSSLLIG 536

QY	441	NRDVGATPANTONYPRAACMDDTITAVNNNSIPETLOKARTWEYTMDSORMDEEDLK	500
Db	537	NRDVGAAITAGGTYYRSCMDSTVTKNNFKIPISVONRYKWTWEYTMHSGMDLDEBLW	596
QY	501	TLPTTVALAIDAVNFSIISKYDLFPKCDOTOMIYDMLRLKSLVYIPGDFVCKKGIGKE	560
Db	597	QLPDKGRDLAIDVANYNISKVALLFGGCDOROMIFDLKRLRSVYLPNDVYCKKGIGRE	656
QY	561	MYIIRKGEVOYLGGPDGTVLTLKAGSVFGEISLIAAGGNRRITANVVAHFANLLTLD	620
Db	657	MYIIQAGOVOLYGGPDGKSVLTLTKAGSVFGEISLIAVGGGNRRITANVVAHFNTLFLD	716
QY	621	KKTLOELLVHYBDSERILMKKARVILLKQAKTAATAPPRKDLALLPPKXEPTKLFKTL	680
Db	717	KKDLLEILLVHYBPESQILRKKARRMIRSNKK-----PKEEKSVLLIPPRAGTKLFFAAL	771
QY	681	GGTGKAS-----LARLLKLKREQAAOKENSEGEBEGKENEKOKENEDKQK	728
Db	772	AMTGMGKGAKGCKLALHRLRLKLEALAEAAKHLEL---VQAAKSQDVKEBEGSAAP	828
QY	729	ENEDKGKE-NEDKDXGREBEKPLDRPECTASPIAV-----EEEPHSVARTVLP	776
Db	829	DQHTPRKEAATPAPAPRTPPEPP-GSPSPSPSPASIGSGEBEGGAPEPESVR-----	882
QY	777	RGTSRQSLIISAPSAEGGEVLTIEVKAKQ	809
Db	883	-----ICMSGPBPBGEOILSVMPPEEREE	906

```

RESULT 4
US-09-949-016-10215
; Sequence 10215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10215
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10215

```

Query Match	20.2%	Score 857	DB 2	Length 698
Best Local Similarity	29.9%	Pred. No. 5.8e-67		
Matches 226	Conservative 153	Mismatches 272	Indels 106	Gaps 22

```

QY      19 INEGRSSRRNEESHHSSNQOQTAAQENKGEESKLTSTPTVYSEEPHTNIQDLSEKSN 78
Db      1 QTEKKAINTQYSHS-----RTHLYVK---TSRDQLNRAENGSLRAHS 41

QY      79 SGDLTTNEDPONAAPTGTVPPEQKEMDPKEGNSPQNKPPAPVINEYADAQNLHLYVKR 138
Db      42 SSEES-----SVLQPGIAMESTRGLADGGQGSFTGQ-----GIATLSKLTFL 83

QY      139 MRQRTALYYKKLVVEGDLSF-----EASPTQAKPLPAVPVKESDDKPTETYYRYLLW 189
Db      84 LRPWAAAHVHQDQGPDSFPRDFRGAELKEVSSQESNAQAVNGSQEPADRG-----RSAW 138

QY      190 FKVKKMPL-----TEYLRKILTPMSI-DSTYDRILYLLMLLVTLAIYNNCWFILP 238
Db      139 -----PLAKCNTNSNNTNEEKTKKKKCAIIVDPSSNIYYRYLTALIAVPFNWLLIC 1922

```

QY	239	RLVPEYQADNIHNLADIICDIILYDMLFIQRLQFVRGDIIVSNELRKXRYST	298
Db	193	RACPELOSEYMLMLVDYDSADVLDVL-VRARGTGLOGLMSDNRMLQHKYIT	251
QY	299	KFOLDVASIIPEDICYLPFFGFN-PMFRANRMLKYSPFEFNHLESIMDKAVIYRIART	357
Db	252	QPKUDVLSVETDYLAKYKGNYPVVRNRLKFSRLFEFFPRTERTRNYPMFRIGNLV	311
QY	358	GYLLEFIILHINACVYYMASNYEGIGITTRWVYDG-----EGNEYLRCYMAVRLLITIG	409
Db	312	LYILIIHMANCIYPAISKFIGFTGDSMWYPIISIEHQRLSRKYISLYXWSTLLTITIG	371
QY	410	GLPEPQITLFEYFOLLNFFSGYFVWSSLIQGMQNDVIGATANQNTFRACMDTIAYMNY	469
Db	372	ETPPPVKDEEYLFVWVDFLVGLIFATIVGNVSMISMNASRAEFOAKIDISIKOYMR	431
QY	470	SIPKLQGRVATWYETWDSQRMIDESDLKTLPTTYQALALADVNFSSISVDFPKGD	529
Db	432	KVYLDLETRVIRWEPYLMANKKYVDEKVLNSLPKLKAELIYNHLDLTKVRIFODE	491
QY	530	TQMITYDMLRLKSVDYLPDGFCKKGEIKGEMYYIKHGEVQYLGAPDGTFTVLTKAGSV	589
Db	492	AGLVELVLTKLPRYPFSGDYICRKGDIQKEMYYINBEKLAIV-ADDGYTQVVLSDGSY	550
QY	590	FGEISLSLAAG--GNRRATANVAHGAFANLLTLDKTLQELIIVHYPDSERIIMTKAR-VL	645
Db	551	FGEISILNTKSGSKGNRRATANIRISIGYDLPCLSKODLMEALTEYPEAKKALEKORQTL	610
QY	646	LKQK---AKTIEATPPRKDALLPPEKKEPKLFTLLGGGKASLARLL-----KL	694
Db	611	MKDNLIDELIRACADPKDL-----EKKVEQLGSSL--DLQTFARFLAEYNATQMOM	662
QY	695	KREQAQAKKENSEGEE--EGKEMEDQKXEMEDKX	728
Db	663	KQRLSQTESQVKGGDKPLADGEVPGDGTK--TEDKQO	698

```

RESULT 5
US-09-538-092-1351
: Sequence 1351, Application US/09538092
: Patent No. 675314
: GENERAL INFORMATION:
: APPLICANT: Gloc, Loic
: APPLICANT: Mansfield, Traci A.
: TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
: FILE REFERENCE: 15966-542
: CURRENT APPLICATION NUMBER: US/09/538,092
: CURRENT FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: 60/127,352
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: 60/178,965
: PRIOR FILING DATE: 2000-02-01
: NUMBER OF SEQ ID NOS: 1387
: SOFTWARE: Curataseqformatter Version 0.9
: SEQ ID NO 1351
: LENGTH: 694
: TYPE: RPT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (0)...(0)
: OTHER INFORMATION: Polypeptide Accession Number Q16281
US-09-538-092-1351

```

Query Match	20.1%	Score 850;	DB 2;	Length 694;
Best Local Similarity	30.0%	Pred. No. 2,46,66;		
Matches 225;	Conservative 149;	Mismatches 269;	Indels 106;	Gaps 22

```

QY      27  NEEGSHPSNQQTAAEENKEEKS.LTKSTPVTSEEHNTIQDKLSKKNSGGDLTNP 866
      | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      5  NTQYSHPS-----RTHLKV-----TSDRLNRAEGLSRHSSSEETS-- 433

```



```

; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1037
; LENGTH: 686
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P29973
US-09-538-092-1037

```

```

Query Match          19.3%; Score 817; DB 2; Length 686;
Best Local Similarity 29.9%; Pred. No. 2e-63;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

```

```

QY 5 LTKVNKVKPIGENNENEGSSRRNEEGSHPS---NOSQOTTAOENKGE-----KSL 53
DB 13 VTMPNVIVP-----DIEKEIRRMENGCASFSEDSDSASTSESENENPHARGSFYSKSL 67
QY 54 KTSSTVTSSEPHNTI QDKLSKNGSGDLTTNPD PONAAPTGTVEQKMDGKGPNS 113
DB 68 R-KGGSQREQYLPGAIALFNVNNS-----NKD-----QEPBEKKKKKKKKSKSDKNE 117
QY 114 POKPPAAPVINEYADAQLNLVKNRORTALYKKKLVBEGDLSPEASPTAKPTAVPV 173
DB 118 NKNDPE-----KKKKKDKKKKK-----E 137
QY 174 KESDDKPTHEYRLMFKYKMPLETKRIKLPNSIDSTDRLYLMLLVL--AYNW 231
DB 138 EKSKDKKEE-----KKEVV-----IDP--SGNTYYNMLFCITLPVWYNW 176
QY 232 NCWFILRLVFPQTADNHNHMLADICDIYLYDMLFIQPLQVRGSDIIVDSNEIR 291
DB 177 T--MVARACFDELQSDYLEYWLIDYVSDIYVLDIM--FVTRTGYLEQGLVKEELKLI 233
QY 292 KHYRTSTKQOLDVASIIPDICYLFFGPN--PMFRANRLKYTSFFFNHLSIMDKAYI 350
DB 234 NKYSNLQRFKLDVLSLIPDILFKLGNNYPEIRLRLRFSMFEPFQRTETRTYVPI 293
QY 351 YEVIRRTGYLFLIHINACVYVWASNYEGIGTRWY-----DGE-----GNEYLRCYYWAV 402
DB 294 FRLSNLWYIVIIHNNACVFSYISKAIGFGNDTWYPPDINDEPRLARKYYSLYWST 353
QY 403 RLITITIGLPEPQTLFEIYFQNLNPFSGVFFVSSSLIGQMRDVI GAATANQNYFRACMDT 462
DB 354 LTLTITIGTPPRPVDSEYVFWVDFLIGVLIFFATIVGNIGSMISNNMAAARAEQARIDAI 413
QY 463 IAYMNNYSIPKLVOKEVRTWYETWDSQRLDESDLKTLPTTQALALADVNFIISKY 522
DB 414 KQYMHRRNYSKOMKEXVIMFEDYLMNKTVDKEVLYKLPDLRAEIALINHLDTLKVY 473
QY 523 DLFGCDTQMIYDMLRLKSVLYLPDGFYCKGGEIGKEMYIIHGEVOYLGGDGTKVLY 582
DB 474 RIFADEAGLIVELVLTQPOVYSPGDYICKKDGIREMYIIKEGLAVV--ADDGVTQFY 532
QY 583 TLKAGSVFGEISLLAAG--GNRRANVAVAGFANLLTLDKKTLOEIIIVHPDSSRIIM 639
DB 533 VLSDSGFGEISITLNTKSGKAGNRRTANIKSIGYSLFCLSKDLMALTEYDADATMLE 592
QY 640 KKAIVLLKOKA-----KTAETPPRKDLALLFPKKEETPKLFTLLGGTGASLARLL--- 662
DB 593 EKGKQILMDGLDLINAINAGSDPKDLEKVTMTMESVDLQF-----RPARILAEV 644
QY 693 -----TLKREQAOKK-----ENSEG--GEEEG 713
DB 645 ESMQKQLKQRLTVEKFLKPLIDTFERSIIEGPAEESG 681

```

RESULT 8
US-09-949-016-11549

```

; Sequence 11549, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11549
; LENGTH: 694
; TYPE: PR
; ORGANISM: Human
US-09-949-016-11549

```

```

Query Match          19.3%; Score 817; DB 2; Length 694;
Best Local Similarity 29.9%; Pred. No. 2e-63;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

```

```

QY 5 LTKVNKVKPIGENNENEGSSRRNEEGSHPS---NOSQOTTAOENKGE-----KSL 53
DB 21 VTMPNVIVP-----DIEKEIRRMENGCASFSEDSDSASTSESENENPHARGSFYSKSL 75
QY 54 KTSSTVTSSEPHNTI QDKLSKNGSGDLTTNPD PONAAPTGTVEQKMDGKGPNS 113
DB 76 R-KGGSQREQYLPGAIALFNVNNS-----NKD-----QEPBEKKKKKKKKSKSDKNE 125
QY 114 POKPPAAPVINEYADAQLNLVKNRORTALYKKKLVBEGDLSPEASPTAKPTAVPV 173
DB 126 NKNDPE-----KKKKKDKKKKK-----E 145
QY 174 KESDDKPTHEYRLMFKYKMPLETKRIKLPNSIDSTDRLYLMLLVL--AYNW 231
DB 146 EKSKDKKEE-----KKEVV-----IDP--SGNTYYNMLFCITLPVWYNW 184
QY 232 NCWFILRLVFPQTADNHNHMLADICDIYLYDMLFIQPLQVRGSDIIVDSNEIR 291
DB 185 T--MVARACFDELQSDYLEYWLIDYVSDIYVLDIM--FVTRTGYLEQGLVKEELKLI 241
QY 292 KHYRTSTKQOLDVASIIPDICYLFFGPN--PMFRANRLKYTSFFFNHLSIMDKAYI 350
DB 242 NKYSNLQRFKLDVLSLIPDILFKLGNNYPEIRLRLRFSMFEPFQRTETRTYVPI 301
QY 351 YEVIRRTGYLFLIHINACVYVWASNYEGIGTRWY-----DGE-----GNEYLRCYYWAV 402
DB 302 FRLSNLWYIVIIHNNACVFSYISKAIGFGNDTWYPPDINDEPRLARKYYSLYWST 361
QY 403 RLITITIGLPEPQTLFEIYFQNLNPFSGVFFVSSSLIGQMRDVI GAATANQNYFRACMDT 462
DB 362 LTLTITIGTPPRPVDSEYVFWVDFLIGVLIFFATIVGNIGSMISNNMAAARAEQARIDAI 421
QY 463 IAYMNNYSIPKLVOKEVRTWYETWDSQRLDESDLKTLPTTQALALADVNFIISKY 522
DB 422 KQYMHRRNYSKOMKEXVIMFEDYLMNKTVDKEVLYKLPDLRAEIALINHLDTLKVY 481
QY 523 DLFGCDTQMIYDMLRLKSVLYLPDGFYCKGGEIGKEMYIIHGEVOYLGGDGTKVLY 582
DB 482 RIFADEAGLIVELVLTQPOVYSPGDYICKKDGIREMYIIKEGLAVV--ADDGVTQFY 540
QY 583 TLKAGSVFGEISLLAAG--GNRRANVAVAGFANLLTLDKKTLOEIIIVHPDSSRIIM 639
DB 541 VLSDSGFGEISITLNTKSGKAGNRRTANIKSIGYSLFCLSKDLMALTEYDADATMLE 600
QY 640 KKAIVLLKOKA-----KTAETPPRKDLALLFPKKEETPKLFTLLGGTGASLARLL--- 692

```

```

Db      601 EKGQILMKDGLDLINANAGSDPKDLBKRVTMEGSDYLLQT-----RFAILAEY 652
QY      693 -----KLRBQAQKK-----ENSEC-GEEEG 713
Db      653 ESMQOKLQRLTKVKFLKPLIDTFSSIEGPAESG 689

RESULT 9
US-09-927-267-1
; Sequence 1, Application US/09927267
; Patent No. 6933147
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG2B: A No. 6933147e1 Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 018512-006510US
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 575
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)
US-09-927-267-1

Query Match      15.5%; Score 655; DB 2; Length 575;
Best Local Similarity 29.2%; Pred. No. 3,7e-49;
Matches 165; Conservative 121; Mismatches 241; Indels 38; Gaps 14;

QY      202 KRIKLPNSIDSYTDRLYLMLLVTLAVNMNCWFPLRLVFPYQADNIHYMLADIICD 261
Db      19 KARKLLPVLDPSGD-YYYWMLNTWFPWVWMLILVCRACFDLOHGIVLAVMLVLDYTS 77
QY      262 ILYYDMLEFIQPLQFVRGSDIIVDSNELRKHYRTSTKQOLDVSAIIPDICYLFFG-FN 320
Db      78 LLYLDMV-VRFHTGFLQGLIVVDKGRISRRVTFWSEFLDLASIMPTDVVYVRIGPHT 136
QY      321 PMFRANRMKXTSFEFNFHLSIMDKATYRVIRRTGGLFILHINACVYMASVYEI 380
Db      137 PTLRLNRFRLAPRLFEAPDRTETRTAYPNAFRIAKMLYIFVVIHNSCLYFALSRYLGP 196
QY      381 GTTRWVYDEG-----NEYLRQYMAVRLTIIGLPEPQTLFEIVFQOLNPFSGVF 432
Db      197 GIDAWYPPPAQGFERLKRQVLYSFYFTLITVGDTPPARBEEYLFWVGDFLLAW 256
QY      433 VPSLLIGQNRDVI-GAATANQNYFRACMDTTA--YNNVSIPLKQKRVRTWYETWDS 489
Db      257 GPATIGSMSSVLYNNMTADAIFY---PDHALVKKTKMLQHVNRKLERVIDWYQHLQIN 313
QY      490 QMLDSDDLKTLPTVQALADIVNFSIISKVDLFRKGDQTOIMVLMRLKSVLRLPG 549
Db      314 KMTNNEVALLOHLEPRLAEVAHSVHLSLTSRVQITONCEASLLEELVTLQPTYSPEG 373
QY      550 FVCKKEIGKEMWYIIGHGEVQVGLGPDGTVLTLVTLKAGSVFGEISLLAAG--GNRRTA 606
Db      374 YVCRKDDIQEWYIIEGQLAIV-ADDGITQYAVLAGLYFGEISIIINIKGMSGNRRTA 432
QY      607 NVVAHGFANILLTDKKTLOEILVHYPDSEIRILMKAR-VLK-----QAKTA--EA 655
Db      433 NIKSLYSDDLFCISKDELEVLSEYPOAQYIMEKREIILKKNKLDVNAEAALIOEA 492
QY      656 TTPRKDALLFPKKEETPKLFTLLGGTGKASLARKLTKRBAQKK-----ENSGGEE 711
Db      493 TESR--LRGIDQDLDTQTFARLLAELESSALKIAYRIERLEWQTRWMPEDLAED 550
QY      712 ECKENEDKQKENDKQKENDKKE 736

```

```

Db      551 EGEPEGTSKDEGRASQEGPPGPE 575

RESULT 10
US-09-927-267-16
; Sequence 16, Application US/09927267
; Patent No. 6933147
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG2B: A No. 6933147e1 Human Cyclic Nucleotide-Gated Ion
; TITLE OF INVENTION: Channel
; FILE REFERENCE: 018512-006510US
; CURRENT APPLICATION NUMBER: US/09/927,267
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/226,253
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 575
; TYPE: PRN
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: rat cyclic nucleotide gated cation channel OCNC2
US-09-927-267-16

Query Match      15.1%; Score 640; DB 2; Length 575;
Best Local Similarity 29.1%; Pred. No. 7,8e-48;
Matches 157; Conservative 114; Mismatches 224; Indels 44; Gaps 13;

QY      218 YLLMLLVTLAVNMNCWFPLRLVFPYQADNIHYMLADIICDIYLYDMLEFIQPLQF 277
Db      34 YWMLNTWFPWVWMLILVCRACFDLOHGIVLAVMLVLDYTSLLYLD-IGVRFHTGF 92
QY      278 VRGSDIIVDSNELRKHYRTSTKQOLDVSAIIPDICYLFFG-FN-PMFRANRMKXTSFE 336
Db      93 LEOGLIVVDKGMIAIRYVRTWSEFLDLASLVPDAAVQGLGPHIPTLRNRFRLVRPLRE 152
QY      337 FNNHLSIMDKATYRVIRRTGGLFILHINACVYMASNYGCIOTTRWVYDEG----- 391
Db      153 AFDRTETRTAYPNAFRIAKMLYIFVVIHNSCLYFALSRYLGFGRDAWVYDDPAQGF 212
QY      392 ---NEYLRQYMAVRLTIIGLPEPQTLFEIVFQOLNPFSGVFSSLLIGQNRDVI-GA 447
Db      213 RLRRQVLYSFYFTLITVGDTPPARBEEYLFWVGDFLLAVMGFATIGSMSSVLYNM 272
QY      448 ATANQNYFRACMDTTA--YNNVSIPLKQKRVRTWYETWDSQRMLESDDLKTLPTT 505
Db      273 NTAADAIFY---PDHALVKKTKMLQHVNRKLERVIDWYQHLQINKMTNEVALLOHLEP 329
QY      506 VOLALADIVNFSIISKVDLFRKGDQTOIMVLMRLKSVLYLGDYFVCKKEIGKEMWYI 565
Db      330 LRAEVAHSVHLSLTSRVQITONCEASLLEELVTLQPTYSGEYVCRGDDIGREMYIIR 389
QY      566 HGEVQVGLGPDGTVLTLVTLKAGSVFGEISLLAAG--GNRRTANVAGFANILLTDK 622
Db      390 EGQLAIV-ADDGITQYAVLAGLYFGEISIIINIKGMSGNRRTANIKSLYSDDLFCISKE 448
QY      623 TLOEILVHYPDSEIRILMKAR-VLK-----QAKTA--EATPRKDALLPKKEE 671
Db      449 DLREVLSEYPOAQYAVEKREIILKKNKLDVNAEAALIOEATSR--LKGIDQDLDD 506
QY      672 TPKLFTLLGGTGKASLARKLTKR-----EQAAQKKEGEBEKEKEDK 719
Db      507 LOTKFAILLAELESSALKIAYRIERLEWQTRWMPEDWEGADDEAPBEGTSKDEBK 565

RESULT 11
US-09-275-252A-18
; Sequence 18, Application US/09275252A

```

```

; Patent No. 664197
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PR
; ORGANISM: Homo sapiens
US-09-275-252A-18

```

```

Query Match          11.4%; Score 484; DB 2; Length 261;
Best Local Similarity 37.2%; Pred. No. 1.6e-34;
Matches 97; Conservative 58; Mismatches 94; Indels 12; Gaps 4;

```

```

QY 370 VYVWASNYEGIGTRRWY---DGE---GNEYLRCYWAVRLLITIGLPEPQTLFEIV 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 IYVAISKSISGFVDVTPYVPIIDPEYGYLARREYVCLYWSLTLLTIGTEPPPVKDEYVL 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 422 FOLLNFSGVFVSSSLIGMRDVGATANQNFRAQMDDTIYMNYSIPKLVQKVRT 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 FVIFDLIGLVITRAITLVGNVSMISNNATRAEQAIDVKKHMQFRKVKSGKEAVIR 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 482 WVEYTWDSQRLDESDLLKPTTVQALADIVNFSIISKVDLFGKCDTOMIYDMLRLK 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 WFDYLTWNTKTVDERELTKLPAKLRRAEININHLSTLKKVRIFHDEAGLVEIVLKL 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 542 SVLYLPGDFVCKKGEIGKEMYYIIKGEVQVVGGBDGTGLVTLKAGSVFGEISLLAAG- 600
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 181 PQVFSFGDYICRKGDIKGEKEMYYIIKEGKLAVV-ADDGVTQVALLSAGSCFGEISILNKGS 239
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 --GNRRTANVVAHGFANLTL 619
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 240 KMGNRRTANIRSLGYSDFCL 260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 12
US-09-270-767-46624
; Sequence 46624, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46624
; LENGTH: 256
; TYPE: PR
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46624

```

```

Query Match          9.8%; Score 416.5; DB 2; Length 256;
Best Local Similarity 36.8%; Pred. No. 1.6e-28;
Matches 78; Conservative 53; Mismatches 80; Indels 1; Gaps 1;

```

```

QY 253 WLADIICDIIVYDMLFIQRLQFVNGDIIIVDSNELRKHVTRSTKFOLDVASIIPDI 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 45 WLACDFPADIIIVLDVFFGHVYVIEFGFWVKNKULTRGVNKRQKFDLLALPLEL 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 313 CYLFFGFNPF-RANRLKTSFEEFNHLESIMDKAYIYVIRITGYLLFIHINACV 371
    ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 105 LYKFLGTQAVWLRFPPFFKIQSFWEVFRLLDRVYSSPHFVRVAKTLTYMLMITHITALY 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 372 YMASNVEGIGTRRWYVDGENEYLRCYMAVRLLITIGLPEPQTLFEIVPOLNFRSGV 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 165 YAVSDVQGLQNKWVSGKHPIYVRCFAFKTATSIKPKRQGEYEVFTVAMLMGV 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 FVFSLSIGMRDVGATANQNFRAQMDDTI 463
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 225 FVFPALLIGQIRDIISRTIRKHKHRYQLEDETL 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 13
US-09-949-016-6615
; Sequence 6615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6615
; LENGTH: 1203
; TYPE: PR
; ORGANISM: Human
US-09-949-016-6615

```

```

Query Match          9.8%; Score 413; DB 2; Length 1203;
Best Local Similarity 23.9%; Pred. No. 3.5e-27;
Matches 152; Conservative 109; Mismatches 273; Indels 101; Gaps 25;

```

```

QY 62 SEBPHTNIQDKLSKN--SSGDLTTNPD--PQNAEPTGTVEQKEMDKGK-----GP 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 SGSSHGHLHDSABERRLIAEGDASPGEDRTPGLAAEPE-----RGASAAQPAASP 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 112 NSPQNKPPAPVINEVADAQNLHLVKKMRQRTAL-YKKLVEGDLSPEASPGTAKPTAV 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 166 PPOQOPPOPASASCEPSVD-----TAKYEGGAADQILPEAEVRLGQAGFM 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 171 PPKVESDDKREHYVLYLWFKVKKMPLTEYLKRIKLPN--SIDSYD-RLYLLMLLVTL 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 215 QRPFGAMLQPGVKKFSLRPFSGQAVERBO-EVKASGAFIITHPYSDFRY--WDLTML 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 228 AYNWNCWFPLRLVPEYQADNIHWMLADIICDIIVYDMLFIQRLQFVNGDIIIVDSNELRKHVTRSTKFOLDVASIIPDI 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 272 LMGVNLIIIPVGITF--FKDENTTPMIVPVVSDTFEFLDLV-----LNFRTGIVVEDNT 324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 282 DIIVDSNELRKHVTRSTKFOLDVASIIPDICL-----FFGFNPMF 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 325 EILLDQRIKMKYKLSW-FWVDFISSIPVDYIFLIVETRIDSVEYKTAARLIVRFTKIL 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 324 RANRMLKTSFEEFNHLESIMDKAY-----IYVIRITGYLLFIHINACVYMASNYE 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 384 SLRLRLRLSLRIYIHQWESIIFHMTYDLSAVVRIYNLIGMMLLCHWDCGLFVPMLO 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 379 GIGTTRW-----VYDGENEYLRCYWAVRLLITIG-GLPEPQTLFEIVPOLNFRSGV 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 444 DFPDDCWVSINNWNVNSWGQYSYALFKAMSHMLCIGYGRQAVGMSDVLTMLSMIVA 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Qy 432 FVSSLLIGOMRDVIGAAATANQYFRAQMDDTIAVNNNYSIPKLQKRVRTWEYTWDSQR 491
Db 504 TCYAMFIGHATALIQSLDSRRQYQEKYQOVMSFHLPPDTRQRIHDYEHRYQG-K 562
Qy 492 MDESDDLKLTPTTQVLAIDVNFSS---ISKVDLFGKCDTOMIYDMLRLKSVLYLPG 548
Db 563 MFDESIILGEISEPLREEL---INFNCRLVASMPLFANADPNFVTSMLTKLRFVFPQG 619
Qy 549 DFVCKKGIGKEMYYIKHGEVOVL-GGPDGTQVLTVLKAGSVFGEISLLAAGGNRRRTAN 607
Db 620 DYIIRREGTIGKMYFIQHGVSVLTKGNKETK----LADGSYFGEICLLTRG---RTAS 672
Qy 608 VVAHGAFANLLTDKKTLOEILVHPDSEIRILMKKA 642
Db 673 VRADTYCRLYSLSVDNFVELEEYP-----MMRRA 702

```

RESULT 14
US-10-067-457-3

Sequence 3, Application US/10067457

Patent No. 6979532

GENERAL INFORMATION:

APPLICANT: Aventis Pharma Deutschland GmbH

TITLE OF INVENTION: Process for identifying substances which modulate the

FILE REFERENCE: AVE D-2000/A006

CURRENT APPLICATION NUMBER: US/10/067,457

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: US/09/779,587

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO. 3

LENGTH: 1203

TYPE: PRT

ORGANISM: Homo sapiens

US-10-067-457-3

Query Match 9.8%; Score 413; DB 2; Length 1203;

Best Local Similarity 23.9%; Pred. No. 3.5e-27;

Matches 152; Conservative 109; Mismatches 273; Indels 101; Gaps 25;

```

Qy 62 SEEPHTNIQDKLSKKN--SSGDLTTPD---PQNAAEPTGVBEQKEMDPGE-----GP 111
Db 115 SSSSHGHLDSEERRLAEGDASPEDCTPPGLAAEP-----RFGASAGPASP 165
Qy 112 NSPQNKPPAPVINEYADQLHNLVKRMQRRL-YKKLVLEGDLSPPASPTAKPTAV 170
Db 166 PPPQPPQPPASASQPSVD-----TAIKVEGGAAGDQILPEAEVRLGQAGPM 214
Qy 171 PPKESDDKPTHYRRLMFKYKXMDLTLYLKRILPN--SIDSTYD-RLYLMLMLLVTL 227
Db 215 QROFAMLOPGVKNKSLRFGSQKAVEREO-ERVSAGFWITHPYSDFEFY--WDLTML 271
Qy 228 AVNANWCWFIPLRVFPYQTADNIHWLADIIDIIYLYDMLFIQRLQFVFG-----G 281
Db 272 LMVGNLIIIPGILTF--PKDENTTPWIVNVSDTFELDIV-----LNFRTGIWVEDT 324
Qy 282 DIIVDSNELKRYRSTKQDLVASTIIPDICYL-----FEGFNPMF 323
Db 325 EIIILPORIKMYKLSM-FMVDFISIPVDYIFLIVETRIDSEVYKTARALIVFTKIL 383
Qy 324 RANRLKYSFPEFNHLESIMDKAY-----YRVARTGYLFIILHINACVYVANSNE 378
Db 384 SLRLRLRSLRIRYHWEELFHMRTDLASAVVRINVLIGMMLLICHMGGCLOFLVPMLO 443
Qy 379 GIGTTRM-----VYDGEENEYLRCCYAAVRLITIG-GLPEPQTLFEIVFOLLNFFSGV 431
Db 444 DFPPDCWVSINNMVNNWNGKQSYALFKAMSHMLCTGYRQAPVGSVDWMLMLSMIVGA 503
Qy 432 FVSSLLIGOMRDVIGAAATANQYFRAQMDDTIAVNNNYSIPKLQKRVRTWEYTWDSQR 491

```

```

Db 504 TCYAMFIGHATALIQSLDSRRQYQEKYQOVMSFHLPPDTRQRIHDYEHRYQG-K 562
Qy 492 MDESDDLKLTPTTQVLAIDVNFSS---ISKVDLFGKCDTOMIYDMLRLKSVLYLPG 548
Db 563 MFDESIILGEISEPLREEL---INFNCRLVASMPLFANADPNFVTSMLTKLRFVFPQG 619
Qy 549 DFVCKKGIGKEMYYIKHGEVOVL-GGPDGTQVLTVLKAGSVFGEISLLAAGGNRRRTAN 607
Db 620 DYIIRREGTIGKMYFIQHGVSVLTKGNKETK----LADGSYFGEICLLTRG---RTAS 672
Qy 608 VVAHGAFANLLTDKKTLOEILVHPDSEIRILMKKA 642
Db 673 VRADTYCRLYSLSVDNFVELEEYP-----MMRRA 702

```

RESULT 15

US-08-997-685A-2

Sequence 2, Application US/08997685A

Patent No. 6551821

GENERAL INFORMATION:

APPLICANT: The Trustees of Columbia University

TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof

FILE REFERENCE: 05/54806

CURRENT APPLICATION NUMBER: US/08/997,685A

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn version 3.1

SEQ ID NO. 2

LENGTH: 910

TYPE: PRT

ORGANISM: mouse

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (130)..(148)

OTHER INFORMATION: S1

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (164)..(185)

OTHER INFORMATION: S2

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (208)..(229)

OTHER INFORMATION: S3

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (243)..(271)

OTHER INFORMATION: S4

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (291)..(313)

OTHER INFORMATION: S5

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (332)..(358)

OTHER INFORMATION: P

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (367)..(387)

OTHER INFORMATION: S6

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (472)..(602)

OTHER INFORMATION: CNB

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: AAC3518

DATABASE ENTRY DATE: 1997-12-27

RELEVANT RESIDUES: (1)..(910)

US-08-997-685A-2

Query Match 9.7%; Score 412.5; DB 2; Length 910;

Best Local Similarity 20.2%; Pred. No. 2.5e-27;

Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, **using frame plus p2n model**

Run on: May 18, 2006, 23:59:38 ; Search time 588 Seconds
(without alignments)
3861.549 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSILTKVKKVXPIGHNEN.....PSAEGEVLITFEKAKQ 809

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 1403666 segs, 935554401 residues
Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model
-Q=/abs/ABSSMBE.spool/US09855828/runat_17052006_181424_25179/app.query.faste_1
-DB=Issued_Patents_NA -QPM=fasteap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -DOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human0.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=plc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-HOST=abes02p -USER=US09855828@CGN 1 1 541@runat_17052006_181424_25179
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents NA:*
- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 - 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 - 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result. being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3594.5	84.9	2135	3	US-09-949-016-1074 Sequence 1074, Ap
2	3575	84.4	2139	3	US-09-949-016-5798 Sequence 5798, Ap
3	857	20.2	3470	3	US-09-949-016-4344 Sequence 4344, Ap
4	817	19.3	2796	3	US-09-949-016-5678 Sequence 5678, Ap
5	748.5	17.7	3266	3	US-09-949-016-16086 Sequence 16086, A
6	692	16.3	84571	3	US-09-949-016-17420 Sequence 17420, A
7	693.5	15.8	2308	3	US-09-927-267-2 Sequence 2, Appl1
8	669	15.8	2366	3	US-09-799-451-351 Sequence 351, App

9	655	15.5	1728	3	US-09-927-267-3 Sequence 3, Appl1
10	560	13.2	601	3	US-09-949-016-38930 Sequence 38930, A
11	560	13.2	601	3	US-09-949-016-205286 Sequence 205286, A
12	560	13.2	99370	3	US-09-949-016-12816 Sequence 12816, A
13	560	13.2	99370	3	US-09-949-016-17540 Sequence 17540, A
14	554	13.1	601	3	US-09-949-016-38931 Sequence 38931, A
15	554	13.1	601	3	US-09-949-016-205287 Sequence 205287, A
16	510.5	12.1	996	3	US-09-270-767-15059 Sequence 15059, A
17	416.5	9.8	4276	3	US-09-949-016-4900 Sequence 4900, Ap
18	416.5	9.8	5065	3	US-09-949-016-744 Sequence 744, App
19	416.5	9.8	5065	4	US-10-067-457-4 Sequence 4, Appl
20	412.5	9.7	2733	3	US-08-997-685A-1 Sequence 1, Appl1
21	406	9.6	3235	3	US-09-949-016-1392 Sequence 1392, Ap
22	406	9.6	3372	3	US-09-949-016-165 Sequence 165, App
23	406	9.6	3372	4	US-10-067-457-2 Sequence 2, Appl1
24	399	9.4	3102	4	US-10-067-457-6 Sequence 6, Appl1
25	382.5	9.0	2246	3	US-09-086-436-38 Sequence 38, Appl
26	382.5	9.0	2263	3	US-08-997-685A-9 Sequence 9, Appl1
27	382.5	9.0	3224	3	US-09-774-528-238 Sequence 238, App
28	382.5	9.0	3224	3	US-10-120-988-238 Sequence 238, App
29	382	9.0	1584	3	US-08-997-685A-3 Sequence 3, Appl1
30	377.5	8.9	1512	3	US-09-086-436-32 Sequence 32, Appl
31	376	8.9	601	3	US-09-949-016-38989 Sequence 38989, A
32	376	8.9	601	3	US-09-949-016-205176 Sequence 205176, A
33	371.5	8.8	2976	3	US-09-774-528-317 Sequence 317, App
34	371.5	8.8	2976	3	US-10-120-988-317 Sequence 317, App
35	368	8.7	1518	3	US-09-086-436-34 Sequence 34, Appl
36	368	8.7	1792	3	US-09-086-436-40 Sequence 40, Appl
37	360.5	8.5	3041	3	US-09-694-777A-19 Sequence 19, Appl
38	350.5	8.3	1507	3	US-08-997-685A-5 Sequence 5, Appl1
39	349	8.2	3041	3	US-09-694-777A-20 Sequence 20, Appl
40	345.5	8.2	2886	3	US-09-694-777A-13 Sequence 13, Appl
41	345.5	8.2	3002	3	US-09-694-777A-11 Sequence 11, Appl1
42	335	7.9	2967	3	US-09-614-480-1 Sequence 1, Appl1
43	335	7.9	2967	3	US-10-162-012-6 Sequence 6, Appl1
44	335	7.9	2967	3	US-10-422-075-1 Sequence 1, Appl1
45	335	7.9	3553	3	US-10-162-012-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-949-016-1074
; Sequence 1074, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1074
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1074
Alignment Scores:
Pred. No.: 0
Score: 3594.50
Percent Similarity: 99.1%
Best Local Similarity: 99.1%
Best Local Similarity: 84.9%
Query Match: 3
DB: Gaps: 1

US-09-855-828-1 (1-809) x US-09-949-016-1074 (1-2135)

QY 114 ProGlnAsnLeuPheProProAlaAlaProValIleAsnGluTyrAlaAspAlaGlnLeuHis 133

Db 1 CCACAAAACAAACCGCTGCAGCTCCTGTTATTAATGAATATGCCATGCCACGCTCAAC 60

QY 134 AsnLeuValIleArgMetArgGlnArgThrAlaLeuTyrIleLysIleLysLeuValGluGly 153

Db 61 AACCTGGTGAAGAAATGGCTCAAGAACAGCCCTTACAGAGAAAAGTTGGTAGAGGA 120

QY 154 AspLeuSerSerProGlnAlaSerProGlnThrAlaLysProThrAlaValProProVal 173

Db 121 GATCTCTCTCCACCCGAAACCCAGCCACCAACTGCAGAAACCCAGCGCTGTACACAGTA 180

QY 174 LysGluSerAspAspLysProThrGluHisTyrTyrArgLeuLeuThrPheLysValLys 193

Db 181 AAGAGAAAGGAGATGAAGCAACAGAACATTAACAAGGCTGTGTGTTCAAAAGTCAAA 240

QY 194 LysMetProLeuThrGluTyrLeuLysArgIleLysLeuProAsnSerIleAspSerTyr 213

Db 241 AAGATGGCTTTAAACAGATACCTTAAGCAATTAACTTCCAAACGATACATTCATAC 300

QY 214 ThrAspArgLeuTyrLeuLeuTyrLeuLeuValThrLeuAlaTyrAsnTyrAsnGly 233

Db 301 ACAGATCGACTATCTCTGTGGCTCTTGCTGTGCTCACTTGCCATTAACCTGAACTGC 360

QY 234 TrpPheIleProLeuArgLeuValPheProTyrGlnThrAlaAspAsnIleHisTyrTrp 253

Db 361 TGTTTTATACCACTGGCTCGCTTCCTTCCATATCAAAACGACAGAACATTAACACTTGG 420

QY 254 LeuIleAlaAspIleIleCysAspIleIleTyrLeuTyrAspMetLeuPheIleGlnPro 273

Db 421 CTTATTTGGCGACATCATATGATATCATCTTATGATATGCTATTTATCCAGCCC 480

QY 274 ArgLeuGlnPheValArgGlyIleValIleValAspSerAsnGluLeuArgLysHis 293

Db 481 AACATCCAGTTTGTAGAGAGAGAGACATTAATGTGATTCAAATGAGCTAAGAGAAACAC 540

QY 294 TyrArgThrSerThrLysPheGlnLeuAspValAlaSerIleIleProPheAspIleCys 313

Db 541 TACAGAGACTTCTCAAAATTTTCAGTTGGATGTGCAATCAATTAATACATTTGATATTTTC 600

QY 314 TyrLeuPhePheGlyIlePheAsnProMetPheArgAlaAsnArgMetLeuLysTyrThrSer 333

Db 601 TACCTCTTCTTGGGTTTAAATCCAAATGTTTAGAGCAATAGCATGTTAAAGTACACTTGA 660

QY 334 PhePheGluPheAsnHisIleLeuGlnSerIleMetAspLysAlaTyrIleTyrArgVal 353

Db 661 TTTTGTGAATTTAATCATCATCACTAGAGTCTATATATGAGCAAAAGCATATATCTACAGATT 720

QY 354 IleArgThrThrGlyTyrLeuLeuPheIleLeuHisIleAsnAlaCysValTyrTyrTrp 373

Db 721 ATTCGAACAACCTGGATTAATGCTGTATTTATCTGCAATTAATGCCGTGTTTATTAATCTGG 780

QY 374 AlaSerAsnTyrGluGlyIleGlyThrThrArgTyrValTyrAspGlyGluGlyAsnGlu 393

Db 781 GCTTCAAACTATACAGAAATGGCACTACTAGATGGGTATATATGGGAGAGAAACGAG 840

QY 394 TyrLeuArgCysTyrTyrTrpAlaValArgThrLeuIleThrIleGlyLeuProGlu 413

Db 841 TATCTAGATGTTATTAATGAGGAGTTGCAACTTTATTAATCAATGTGTGCTTCCAGAA 900

QY 414 ProGlnThrLeuPheGluIleValPheGlnLeuLeuAsnPhePheSerGlyValPheVal 433

Db 901 CCACAAACTTATTTAAATGTGTTTCAACTCTTAATTTTCTTGGAGTTTGTG 960

QY 434 PheSerSerLeuIleGlyGlnMetArgAspValIleGlyAlaAlaThrAlaAsnGlnAsn 453

Db 961 TTCTCCAGTTTATATGGTACGATGAGATGTCAATGAGACACTACAGCCAAATCCGAAC 1020

QY 454 TyrPheArgAlaCysMetAspSerThrIleAlaTyrMetAsnAsnTyrSerIleProLys 473

Db 1021 TACTTCCGCGCTGCATGATGACACCATTCGCTAATGAACTAATCTCATTCCTTAAA 1080

QY 474 LeuValGlnLysArgValArgThrTyrPlyGlyTyrThrTrpAspSerGlnArgMetLeu 493

Db 1081 CTTTGCAAAACCGAGTTCGAGCTTGATGAAATTAATACATGGGACTCTCAAAAGAAATGCTA 1140

QY 494 AspGluSerAspLeuLeuLysThrLeuProThrThrValGlnLeuAlaLeuAlaIleAsp 513

Db 1141 GATGAGTCTGATTTCTTAAAGACCTTACCACTAGCGTCCAGTTAGCCCTCCCAATTGAT 1200

QY 514 ValAsnPheSerIleIleSerLysValAspLeuPheLysGlyCysAspThrGlnMetIle 533

Db 1201 GTAACTTCAGCATATATAGCAAAATGATATCATCAAGCATGAGAAATCCAAATGTTCTGGA 1260

QY 534 TyrAspMetLeuLeuArgLeuLysSerValLeuTyrLeuProGlyAspPheValCysLys 553

Db 1261 TATGACATGTTCTTAAGATGAAATCCGTTCTATTTCCCTGGTGACTTGTCTGCAAA 1320

QY 554 LysGlyGlnIleGlyLysGlnMetTyrIleIleLysHisGlyGluValGlnValLeuGly 573

Db 1321 AAGGAGAAATGGCAAGAAATGATATCATCAAGCATGAGAAATCCAAATGTTCTGGA 1380

QY 574 GlyProAspGlyThrLysValLeuValThrLeuLysAlaGlySerValPheGlyGluIle 593

Db 1381 GGCCCTGATGTACTTAAAGTTCTGTGTACTGAAAGCTGGGTCCGTC----- 1428

QY 594 SerLeuLeuAlaAlaGlyGlyLysAsnArgArgThrAlaAsnValValAlaHisGlyPhe 613

Db 1429 ---CTTTCAGCAGCAGAGAGAGAAACCGTCGAACCTGCCAAATGTGTGGCCACCGGTTT 1485

QY 614 AlaAsnLeuLeuThrLeuAspLysLysThrLeuGlnIleLeuValHisTyrProAsp 633

Db 1486 GCCAATCTTTTAACCTAGACAAAAAGCCCTCCAAAGAAATCTAGTGATTAATCCAGAT 1545

QY 634 SerGluArgIleLeuMetLysLysAlaArgValIleLeuLysGlnLysAlaLysThrAla 653

Db 1546 TCTGAAGAGATCCTCATGAAGAAACCGAGAGCTTTTAAACAGAGCTTAAGACCGGA 1605

QY 654 GluAlaThrProProArgLysAspLeuAlaLeuLeuPheProProLysGlnGluThrPro 673

Db 1606 GAAAGCAACCCCTCCAGAGAAAGATCTTGCCCTCTCTCCACCGAAAGAAAGACACCC 1665

QY 674 LysLeuPheLysThrLeuLeuGlyGlyThrGlyLysAlaSerLeuAlaArgLeuLeuLys 693

Db 1666 AAATGTTTAAACCTCTCTAGAGAGCAGAGAAAGCAAGCTTGCAAGACTACTCAAA 1725

QY 694 LeuLysArgGluGlnAlaAlaGlnLysLysGluAsnSerGluGlyGluGluGluGly 713

Db 1726 TTGAAGCGAGACCAAGCACTCAGAAAGAAATTTCTGAAGAGAGAGAGAGAGAGGA 1785

QY 714 LysGluAsnGluAspLysGlnLysGluAsnGluAspLysGlnLysGlnLysAsnGluAspLys 733

Db 1786 AAGAGAAATGAAGATTAACAAAGAAATGAAGATTAACAAAGAAATGAAGATTAAG 1845

QY 734 GlyLysGluAsnGluAspLysAspLysGlyArgGluProGluGluLysProLeuAspArg 753

Db 1846 GGAAGAAAGAAATGAAGATTAAGATTAAGAGAAAGAGCCAGAGAGAGACCACTGACAGA 1905

QY 754 ProGluCysThrAlaSerProIleAlaValGluGluGluProHisSerValArgArgThr 773

Db 1906 CCTGAATGTACAGCAAGTCTTATGCAGTGAGAGAAAGAAACCCCACTCAATTTGAAGAGCA 1965

QY 774 ValLeuProArgGlyThrSerArgInsLeuIleIleSerMetAlaProSerAlaGln 793

Db 1966 GTTTTACCAAGAGGACTTCTGTCATATCATCATTTATAGCATGGCTCTTCTGCTGAG 2025

QY 794 GlyGlyGluGluValLeuThrIleGluValLysGluLysAlaLysGln 809

Db 2026 GCGGAGAGAGAGTTCTTACTATTGAAGTCAAGAAAGAAAGCTAAGCAA 2073

RESULT 2
US-09-949-016-5798
; Sequence 5798, Application US/09949016


```

Db      1666 ACCCAAACTGTTAAAACTCTCTCTAGAGGCAACAGAAAAAGCAAGTCTTGCAAGACTACT 1725
Qy      692 ULysLeuYsArGluGlnAlaGlnLysLysGluAsnSerGlnGlyGluGluGln 712
Db      1726 CAAATTGAGCGACAGACAGACGCTCCAGAGAAAAGAAATTTCTGAGAGGAGAGAGAGA 1785
Qy      712 uGlyLysGluAsnGluAspLysGlnLysGluAsnGluAspLysGlnLysGluAsnGluAs 732
Db      1786 AGGAAAAGAAATGAAGATTAACAAAAAGAAATGAGATTAACAAAAAGAAATGAAGA 1845
Qy      732 pLySgLyLysGluAsnGluAspLysGlnLysGluGluProGluGluLysProLeuAs 752
Db      1846 TAAAGAAAAAGAAATGAAGATTAACAAAAAGAGCCAGAGCAAGAACCCCTGGA 1905
Qy      752 PARProGluCysThrAlaSerProIleAlaGluGluGluProHisSerValArgAr 772
Db      1906 CAGACCTGAATGACAGCAAGTCTTCTTCAGTGGAGAGAAACCCCACTTCAGTTGAAG 1965
Qy      772 gThrValLeuProArgGlyThrSerArgLysSerLeuIleIleSerMetAlaProSerAl 792
Db      1966 GACAGTTTACCAGAGGAGGACTTCTGTCATCAGCTCATTAACAGCATGGCTCTCTGC 2025
Qy      792 aGluGlyGlyGluGluValLeuThrIleGluValLysGluLysAlaLysGln 809
Db      2026 TGAGGCGGAGAGAGAGTCTTACTATTGAAGTCAAAAGAAAGGCTAAAGCAA 2077

```

```

RESULT 3
US-09-949-016-4344
; Sequence 4344: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4344
; LENGTH: 3470
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4344

```

```

Alignment Scores:
Pred. No.: 2,796-85 Length: 3470
Score: 857.00 Matches: 226
Percent Similarity: 50.1% Conservative: 153
Best Local Similarity: 29.9% Mismatches: 272
Query Match: 20.2% Indels: 106
DB: 3 Gaps: 22

```

```

US-09-855-828-1 (1-809) x US-09-949-016-4344 (1-3470)
Qy      19 GluAsnGluGlnSerSerArgArGAsnGluGluGlySerHisProSerAsnGlnSerGln 38
Db      28 CAAACCGAGAAAGTGGCCAAAGATCAACACCCAACTCCACCCCTCC----- 75
Qy      39 GlnThrThrAlaGlnGluGluAsnLysGlyGluGluLysSerLeuLysThrLysSerThr 58
Db      76 -----AGAACCCACCTCAAGGTAAAG----- 96
Qy      59 ProValThrSerGluGluProHisThrAsnIleGluAspLysLeuSerLysAsnSer 78
Db      97 -----ACCTCAGACCGAGATCTCAATCGCGCTGAAAAATGGCCTCAGCAGAGCCCACTCG 150

```

```

Qy      79 SerGlyAspLeuThrThrAsnProAspProGlnAsnAlaAlaGluProThrGlyThrVal 98
Db      151 TCAAGTGAAGAGACATCG-----TCAGTGTCTGACACCG---GGGATCGCC 192
Qy      99 ProGluGlnLysGluMetAspProGlyLysGluGlyProHisSerProGlnAsnLysPro 118
Db      193 ATGAGACCAAGAGCATGGCTGACTCCGGCGGGCTCTTCAACGGGCCAG----- 243
Qy      119 ProAlaIleProValIleAsnGluThrAlaAspAlaGlnLeuHisAsnLeuValLysArg 138
Db      244 -----GGGATCGCCAGGCTGTCCGGCTCATCTTCTTG 276
Qy      139 MetArgGlnArgThrAlaLeuThrLysLysLysLeuValGlnGlyAspLeuSerSerPro 158
Db      277 CTGCCAGGTGGGCTGCCAGGATGTGCACCCAGACACAGGACCGGACCTCTTCTCT 336
Qy      159 -----GluAsnProGlnThrAlaLysProThrAla 169
Db      337 GATCGTTTCCGTGAGCCGAGCTTAAGAGGTGTCCAGCCAAAGAAAGCAATGCCAGGCA 396
Qy      170 ValProValLysGluSerAspAspLysProThrGlnHisIleThrArgLeuLeuThr 189
Db      397 AATGTGGCGAGCCAGAGAGCCAGACACAGAGG-----AGAGCGGCTTG 441
Qy      190 PheLysValLysLysMetProLeu-----ThrGlu 199
Db      442 -----CCCTGGCCAAATGCACACTAACCCAGCAACACAGGAG 483
Qy      200 TyrLeuLysArgIleLysLeuProAsnSerIle---AspSerThrThrAspArgLeuThr 218
Db      484 GAGGAGAAAGAAAGAGAAAGAGAGATGGATGTGTGGAGCCCTCCAGCAACCTGTAC 543
Qy      219 LeuLeuThrLeuLeuValThrLeuAlaTyrAsnThrAsnCysThrPheIleProLeu 238
Db      544 TACCGGTGCTACCGGCATCGCCCTGCTCTTAACTGAGATCGCTTATTATTC 603
Qy      239 ArgLeuValPheProTyrGlnThrAlaAspAsnIleHisIleThrLeuIleAlaAspIle 258
Db      604 AGGGCGCTGTTTGATGAGTGCAGTCCGAGTACCTGATGCTGTGGCTGTGCTGAGCTAC 663
Qy      259 IleCysAspIleIleTyrLeuThrAspMetLeuPheIleGlnProArgLeuGlnPheVal 278
Db      664 TCGGAGATGCTGATGTCTTGGATGCTT---GAGAGCTGAGCAGATTTC 720
Qy      279 ArgGlyGlyAspIleLeuValAspSerAsnGluLeuArgLysHisIleThrArgThrSerThr 298
Db      721 GAGCAAGGCTTAAGTCAAGTATACCAACAGGCTGTCAGACATTAACAGACAGACAG 780
Qy      299 LysPheGlnLeuAspValAlaSerIleIleProPheAspIleCysTyrLeuPhePheGly 318
Db      781 CAGTTCAAGCTGATGTGTTGCTCCGTGCTCCAGCTGAGCTTAAAGGTGGGC 840
Qy      319 PheAsn---PrometPheArgAlaAsnArgMetLeuLysTyrThrSerPhePheGluPhe 337
Db      841 ACDAATACCAGAAAGTGAAGTTCAACGCGCTACAGAAATTTTCCGGCGCTTTGAATTC 900
Qy      338 AsnHisIleLeuGlnSerIleMetAspLysAlaTyrIleTyrArgValIleArgThrThr 357
Db      901 TTTCAGCCGACAGAGACAGAGCAAGCAACATCCCAATATGTCAGATGGGAACTTGTC 960
Qy      358 GlyTyrLeuLeuPheIleLeuHisIleAsnAlaCysValTyrTyrThrAlaSerAsnTyr 377
Db      961 TTGTCAATTCATCATCTATCTCACTGAGATGGCTGATCTTATTCATTTCCAGATTC 1020
Qy      378 GluGlyIleGlyThrThrArgThrValTyrAspGly----- 389
Db      1021 ATTTGTTTGGAGCAAGCTCTGGGTCTCCCAACATGTCATCCCAAGCATGGGCGC 1080
Qy      390 GluGlyAsnGlyTyrLeuArgCysTyrTyrThrAlaValArgThrLeuIleThrIleGly 409
Db      1081 CTCTCCAGAGATGATATTACAGTCTCTACTGCTGACCTTACACCATTTGG 1140
Qy      410 GlyLeuProGluProGlnThrLeuPheGluIleValPheGlnLeuLeuAsnPhePheSer 429

```

```

Db      1141 GAGACCCACCCCGGAAAGATGAGGATATCTCTTTGTCGAGACTTCTGCTG
Qy      430 GYVALPheValPheSerLeuIleGlyIleMetArgValIleGlyIleAlaThr
Db      1201 GGTGTTCTGATTTTTCACCATTTGGGCAATGGCTCCATGATCTCGAATATGAAAT
Qy      450 ALaSerGlnAsnThrPheArgAlaCysMetAspAspThrIleAlaThrMetLanAsnThr
Db      1261 GCCTCAGGCGACAGATTCCAGCCAAAGATTGATTCATCAAGACATGACAGTTCCGC
Qy      470 SerIleProIleValGlnIleValArgValArgThrTrpIleGlyIleThrTrpAspSer
Db      1321 AAGGTACCAAGAGACTTGGAGACGCGGTTATCCGGTGTTGACTACTACCTGTGGGCAAC
Qy      490 GlnArgMetLeuAspGluSerAspLeuLeuIleThrLeuProThrThrValGlnLeuAla
Db      1381 AAGAAACGCGTATGAGAAGAGGAGTGCTCAAGACCTCCCAAGACAGTGAAGGCTGAG
Qy      510 LeuAlaIleAspValAsnPheSerIleIleSerIleValAspLeuPheIleGlyIleAsp
Db      1441 ATCGGCATCAACCTGACCTCGACACGCTGAAGAGAGTTGCAATCTTCCAGAGCTGTGAG
Qy      530 ThrGlnMetIleThrAspMetLeuLeuArgLeuIleIleValLeuIleuThrProGlyIleAsp
Db      1501 GCAGGCGCTGCTGTGAGCTGCTGCTGAGAGCTGCAACCCATGCTGTTACAGCCCTGGGGAT
Qy      550 PheValCysLeuIleGlyIleGlyIleGlyIleGlyIleMetIleIleIleIleIleIleIle
Db      1561 TTTATCTGCAAGAGAGGAGATATTTGGAGAGGAGATGATCATCAACAGAGGCAAGCTG
Qy      570 GlnValIleGlyIleProAspGlyIleThrIleValLeuValThrLeuIleIleGlyIleVal
Db      1621 GCCCTGCTG---GCTATGATGGGTCACCCAGCTTGTGCTCTCAAGCATGCGACGTAC
Qy      590 PheGlyIleIleSerLeuLeuAlaIleGlyIle-----GlyAsnArgAlaThrAla
Db      1678 TTCGGGAGATCAGCATCTTCAACATCAAGGAGCAAGTCCGGGAACCCAGAGAGGCC
Qy      607 AsnValValAlaIleGlyIleAlaAsnLeuLeuThrLeuAspIleIleGlyIleGlyIle
Db      1738 AACATCGGACATTTGGCTACTAGACCTGTTCTGCTCTCAAGAGACATCTCATGAGAG
Qy      627 IleLeuValIleThrProAspSerGluArgIleLeuMetIleIleIleIleIleIleIle
Db      1798 GCCCTACCGAGTACCCCGAAGCAAGAGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAG
Qy      646 LeuIleGlnIleIle-----AlaIleThrAlaGlnAlaIleThrProAspArgIleAspLeu
Db      1858 ATGAAGAGACAACTGATGATGAGAGCTGCGCAGGCGCGGCGCGGAGAGAGAGAGAGAG
Qy      663 AlaLeuLeuPheProIleProIleGlyIleThrProIlePheIleThrLeuLeuIleGly
Db      1918 -----GAGGAGAAAGTGAAGCACTGGGCTGCTCCCTG-----GAGC
Qy      683 ThrGlyIleAlaSerLeuAlaArgLeuLeu-----IleLeu
Db      1954 ACCCTCAGACCAAGTTTTCAGCCCTCTGCTGCTGAGTACAAAGCCCAAGATGAAGATG
Qy      695 LysArgGlnGlnAlaIleGlnIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      2014 AAGCAGCGTCTGACCACTGCAAGACCAAGGTGAAGGTGTGTGGGACAAAGCCCTGGCT
Qy      712 GlnGlyIleGlnIleAsnIleAspIleGlyIleGlnIleGlnIleGlnIleGlnIle
Db      2074 GATGGGGAAGTTCCCGGGGATGCTACAAA---ACAGAGAGCAAAACAGAG 2121

```

```

RESULT 4
US-09-949-016-5678
; Sequence 5678; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5678
; LENGTH: 2796
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5678

Alignment Scores:
Pred. No.: 6,15e-81 Length: 2796
Score: 817.00 Matches: 226
Percent Similarity: 46.9% Conservative: 129
Best Local Similarity: 29.9% Mismatches: 266
Query Match: 19.3% Indels: 136
DB: 3 Gaps: 24

US-09-855-828-1 (1-809) x US-09-949-016-5678 (1-2796)
Qy      5 LeuThrIleValAsnIleValIleProIleGlyIleAsnAsnGlnIleGlnIleSer
Db      365 GTTACCATCCCAATGTGATTGATCA-----GATATTGAAAAGAAATA
Qy      25 ArgArgAsnGlnIleGlyIleSerIleIleProSer-----AsnIleSerGlnIleThr
Db      410 CGAAGATGAAATCAATGACATGACATGCTCTTTCTGAGGATGATGACAGTGCCTTACA
Qy      41 ThrAlaGlnGlnIleGlnIleGlnIleGlnIle-----LysSerLeu
Db      470 TCGAAGAAATCAAGAGATGAAACCTCATGCAAGGGGCTTCTTAAATTAAATGATCCTC
Qy      54 LysThrIleSerThrProValThrSerGlnIleProIleThrAsnIleGlnIleAspIleu
Db      530 AGA---AAGGAGACCATCAACAGAGGAGACAGTACCTGCTGCTGCTGCTGCTGCTGCTG
Qy      74 SerLysLysAsnSerSerGlyAspLeuThrThrAsnProAspProGlnIleAsnAlaIleGly
Db      587 AATGTGAACAACAGCAGC-----AATTAAGAC-----CAGGA
Qy      94 ProThrGlyIleThrValProIleGlnIleGlnIleMetAspProGlyIleGlnIleProAsnSer
Db      620 CCAGAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA
Qy      114 ProGlnAsnIleProProIleAlaIleProValIleAsnGlyIleAlaIleAspIleIleIle
Db      680 AATTAAGAAAGACCCAGAG-----
Qy      134 AsnLeuValIleAsnIleArgIleArgIleArgIleArgIleArgIleArgIleArgIleArg
Db      698 -----AAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA
Qy      154 AspLeuSerSerProGlnIleAspProGlnIleThrAlaIleProIleProIleProIle
Db      737 -----GAG
Qy      174 LysGluSerAspAspIleProIleThrGlnIleIleIleIleIleIleIleIleIleIleIle
Db      740 GAGAAAAGCAAGATTAAGAAAAGAGAG-----AAG
Qy      194 LysMetProLeuThrGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      773 AAAAGAAATGTGTGTT-----ATTGATCCC-----796

```

```

QY 214 ThrAspArgLeuTyrLeuLeuThrLeu-----AlaTyrAsnTP 231
DB 797 TCGGAACACATATATACACTGGCTTTTGCATCACAATTCCTTATGACAACTGG 856
QY 232 AsnCySTPrPheIleProLeuArgLeuValPheProTyrGlnThrAlaAspAsnIleHis 251
DB 857 ACA-----ATGGTTATTCGCCAGAGCATGTTTGTGAACCTTCATTCGATTAACCTAGAA 910
QY 252 TTTTPrLeuIleAlaAspIleIleCysAspIleIleTyrLeuTyrAspMetLeuPheIle 271
DB 911 TATTCGCTCATTTGGATTAAGTATCAGACATAGCTATTTATTAATGATATG---TTTGTGA 967
QY 272 GlnProArgLeuGlnPheValArgGlyAspIleIleValAspSerAsnGlnLeuArg 291
DB 968 CCAACAGAGCAGAGGTACTACAGAACAGAGCAGCTGCTGAAGAGAACTTAAGCTCATA 1027
QY 292 LysHisTyrArgThrSerThrLysPheGlnLeuAspValAlaSerIleIleProPheAsp 311
DB 1028 AATAAATATATAATCCAACTTGCAATTTAAACTTGATGTTCTGCACTGATACCACTGAT 1087
QY 312 IleCysTyrLeuPhePheGlyPheAsn---PrometPheArgAlaAsnArgMetLeuLys 330
DB 1088 TTGCTGATATTTTAAGTTAGGGGTGAACCTATCCAGAAATTAGATTAAACAGGTTGTTACGG 1147
QY 331 TyrThrSerPhePheGlnPheAsnHisIleGlnSerIleMetAspLysAlaTyrIle 350
DB 1148 TTCTCTCGATGTTTGAGTTCTTCCAGAGAACAGAAACAAGAGCAAACTATCCAAACATC 1207
QY 351 TyrArgValIleArgThrThrGlyTyrLeuLeuPheIleLeuHisIleAsnAlaCysVal 370
DB 1208 TTCAGAGATTCCAAACCTTGTTATGTAATATCGTCATCATTAATCCACGAGATGATGTG 1267
QY 371 TyrTyrTyrPheAspSerAsnTyrGlnGlyIleGlyThrThrArgTyrValTyr----- 387
DB 1268 TTCTACTCTATTTCTTAAAGCTATGAGATTGGAAATGATACATGGTCTTACCTGATATT 1327
QY 388 ---AspGlyGlu-----GlyAsnGlnTyrLeuArgCysTyrTyrTyrPheAlaVal 402
DB 1328 AATGATCCTGAAATTTGGCCGTTTGGCTAGAAATAATGATTAACAGCCTTTACTGCTGAC 1387
QY 403 ArgThrLeuIleThrIleGlyLeuProGlnProGlnThrLeuPheGlnIleValPhe 422
DB 1388 CTGACTTACTACCACTTGCTGTGAACACCCCTCCGCTGAGGGATTCGATGATGCTTT 1447
QY 423 GlnLeuLeuAsnPhePheSerGlyValPheValPheSerSerIleGlyGlnMetArg 442
DB 1448 GTGGTGCTGATTTCTTAATGAGAGTTTAATTTTGTCTACCACTGCTGTAACATAGGT 1507
QY 443 AspValIleGlyAlaAlaThrAlaAsnGlnAsnTyrPheArgAlaCysMetAspAspThr 462
DB 1508 TCTATGATTTCCAAACATGATGAGCAGCAGAGCAAGATTTCAACAGAAATGATGCTATC 1567
QY 463 IleAlaTyrMetAsnAsnTyrSerIleProLysLeuValGlnLysArgValArgThrTP 482
DB 1568 AAGCAATATATGATTTTCGAAATGTAAAGCAAGATATGAAAGAGGGTATTATTAATG 1627
QY 483 TyrGlnTyrThrTyrAspSerGlnArgMetLeuAspGlnSerAspLeuLeuTyrThrLeu 502
DB 1628 TTGGACTACTGCTGGACCAACAAAAAAAGCTTGATGAGAAAGAAAGCTTTAAAGTATCTA 1687
QY 503 ProThrThrValGlnLeuAlaLeuAlaIleAspValAsnPheSerIleIleSerLysVal 522
DB 1688 CCTGATTAACCTAGACAGCAAAATTTGCCATCAACGTTTACATTAACATTAATAAAGATA 1747
QY 523 AspLeuPheLysGlyCysAspThrGlnMetIleTyrAspMetLeuLeuArgLeuLysSer 542
DB 1748 CGCATTTTGTCTGATTTGCTGAAGCTGCTGTTGCTGAGAGTTGCTTGAATAATGCAACC 1807
QY 543 ValLeuTyrLeuProGlyAspPheValCysLysLysGlyGlnIleGlyLysGlnMetTyr 562
DB 1808 CAAGTCTACAGTCTCTGAGATATATATTGCAAAAGAGGATATCGACAGACAGATGTAC 1867
QY 563 IleIleLysHisGlyGlnValGlnValLeuGlyLysProAspGlyThrLysValLeuVal 582

```

```

DB 1868 ATTATCAAGAAAGCAAACTGCTGTGGTG---GCAGATGATGAGTCACTCAGTTTGTG 1924
QY 583 ThrLeuLysAlaGlySerValPheGlyGlnIleSerLeuLeuAlaAlaGlyIle----- 600
DB 1925 GTATTGACCGATGGAGCTACTTCGCTGAGATCAGCATTTCTTTACATTAAAGGAGCAAA 1984
QY 601 ---GlyAsnArgArgThrAlaAsnValAlaHisGlyPheAlaAsnLeuLeuThrLeu 619
DB 1985 GGTGGCATTCGAAGAACGCCCAATATTAAGATATTTAGCTACTACAGACTGTTCTGTCTC 2044
QY 620 AspLysLysThrLeuGlnGlnIleLeuValHisTyrProAspSerGlnArgIleLeuMet 639
DB 2045 TCAAAAGTGAACCTCATGAGAGCTTAACCTGAGTACCAAGATCCAAACATATGCTGAA 2104
QY 640 LysLysAlaArgValLeuLeuLysGlnLysAla-----LysThrAlaGlnAla 655
DB 2105 GAGAAAGGAGACAGATTTTAATGAAGATGCTCTAATCGATCTAAACATTGCCAAATGCT 2164
QY 656 ThrProProArgLysAspLeuAlaLeuLeuPheProProLysGlnGlnThrProLysLeu 675
DB 2165 GGCAGTGAATCCTAAAGATCTTGAAGAGATGCTTACGATTCGAATGAGAGGGTCACTAGACCTC 2224
QY 676 PheLysThrLeuLeuGlyGlyTyrGlyLysAlaSerLeuAlaArgLeuLeu----- 692
DB 2225 CTGCAAAACC-----AGCTTTGCCGAATCTTGCTGATGAT 2260
QY 693 -----LysLeuLysArgGlnGlnAlaIleGlnLysLys----- 703
DB 2261 GAGTCCATGACAGCAAACTGAAACAAAGATTAAACCAAGTTTGTGAAACCG 2320
QY 704 -----GlnAsnSerGlnGly---GlyGlnGlnGlnGly 713
DB 2321 CTATTTGACACAGAAATTTCAAGTATGTAGGAGCACTGGACGGAAGTGGG 2371

RESULT 5
US-09-949-016-16086
; Sequence 16086, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16086
; LENGTH: 32666
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16086

Alignment Scores:
Pred. No.: 2,44e-71 Length: 32666
Score: 748.50 Matches: 167
Percent Similarity: 57.2% Conservative: 108
Best Local Similarity: 34.7% Mismatches: 169
Query Match: 17.7% Indels: 37
DB: 3 Gaps: 11

US-09-855-828-1 (1-809) x US-09-949-016-16086 (1-32666)
QY 275 LeuGlnPheValArgGlyAspIleIleValAspSerAsnGlnLeuLysHisTyr 294
DB 27904 TTAGGTTTCTCGAGCAGAGCTTTAATGTCATGATATCCAAACAGGCTGTGGCAGCATTTAC 27963

```


QY 178 AspLysProThrGluHisIleTyrArgLeuLeuTrpPheValIleValSlyMetProLeu 197
 DB 417 -----CCATCTGGGATTACTAC-----TACTGG----- 440
 QY 198 ThrGluTyrLeuLysArgIleLeuLeuProAsnSerIleAspSerTyrThrAspArgLeu 217
 DB 440 ----- 440
 QY 218 TyrLeuLeuTrpLeuLeuValThrLeuAlaTyrAsnTrpAsnCySTrpPheIlePro 237
 DB 441 -----TGGCTGAACACAAATGGTCTTCCCATCATGTATTAACCTCATCATCTCTGGT 491
 QY 238 LeuArgLeuValPheProTyrGlnThrAlaAspAsnIleHisTyrTrpLeuIleAlaAsp 257
 DB 492 TGCAGAGCCCTGCTCCCGCATTCGACACGCGTTATGTGGTGGCTGGTGGCTGGAC 551
 QY 258 IleIleCysAspIleIleTyrLeuTyrAspMetLeuPheIleGlnProArgLeuGlnPhe 277
 DB 552 TACACGAGTGAACCTGATACCTACTAGACATGGTG---GTGGCTTCCACACAGAGATTC 608
 QY 278 ValArgGlyIleValAspIleIleValAspSerAsnGlnLeuArgIleSlyTyrArgThrSer 297
 DB 609 TTGAACACGGGATCTCTGGTGGTGAACAGGTAAGATCTGAGTCCGATCGTTCCGAC 668
 QY 298 ThrLysPheGlnLeuAspValAlaSerIleIleProPheAspIleCySTyrLeuPhePhe 317
 DB 669 TGGAGTTTCTTCTTGGACCTGGCTTCCCTGATGCCCCACAGATGGCTACGTCGGCTG 728
 QY 318 Gly---PheAsnProMetPheArgAlaAsnArgMetLeuLysTyrThrSerPhePheGln 336
 DB 729 GGGCCGACACACCCACCCGAGGCTGAAACCGCTTCTCCGCGGCCCCCCTCTTGAG 788
 QY 337 PheAsnHisIleLeuGlnSerIleMetAspLysAlaIleTyrArgValIleArgThr 356
 DB 789 GCCTTGACCCGACAGACCCGACAGCTTACCCAAATGCTTGGCATTTGCCAATGCCAGCTG 848
 QY 357 ThrGlyTyrLeuLeuPheIleLeuHisIleAsnAlaCysValTyrTyrTrpAlaSerAsn 376
 DB 849 ATGCTTTACATTTTTCGTCATCCATTCGAAACAGCTGCTTATCTTGGCCCTATCCCG 908
 QY 377 TyrGluGlyIleGlyThrThrArgTrpValTyrAspGlyGln 391
 DB 909 TACCTGGGCTTCCGGGCTGACGATGGGTGATCCCGGACCCCGACGCTGGCTTGGAG 968
 QY 392 -----AsnGlnTyrLeuArgCysTyrTyrTrpAlaValArgThrIle 408
 DB 969 CGCTCGCGGCGGACGATCTCTAGCTTTTACTTCTCCACGCTGATAGCTACTACAGTG 1028
 QY 409 GlyGlyLeuProGlnProGlnThrLeuPheGlnIleValPheGlnLeuLeuAsnPhePhe 428
 DB 1029 GGGGATACACCGCCCGACGAGGAAGAAGATACCTTTCATGTGGGCGACTTCTCG 1088
 QY 429 SerGlyValPheValPheSerSerLeuIleGlyIleMetArgAspValIle---GlyAla 447
 DB 1089 CTGGCGCTCATGGGTTTCCGACCATCATGGTAGCATGCTGTCATCTACACATG 1148
 QY 448 AlaThrAlaAsnGlnAsnTyrPheArgAlaCysMetAspSerPheIleAla-----Tyr 465
 DB 1149 AACACTGACAGTCCGGCTTCTTAC-----CCAAATCATGCACGCTGAAGAAATAC 1199
 QY 466 MetAsnAsnTyrSerIleProLysLeuValGlnLysArgValArgThrTyrGlyTyr 485
 DB 1200 ATGAAGCTGACGACGTCACACCCGACGCTGACGGGAGATTATGTACGTATCAGAC 1259
 QY 486 ThrTrpAspSerGlnArgMetLeuAspGlnSerAspLeuLysThrLeuProThrThr 505
 DB 1260 CTCACAGTCAACAAGAAATGACCAACAGAGTAGCCATCTTACAGACCTTGCTGAGCGG 1319
 QY 506 ValGlnLeuAlaLeuAlaIleAspValAsnPheSerIleIleSerLysValAspLeuPhe 525
 DB 1320 CTCGGGCGACAAAGTGTGTCTGCTGACCTGTCCTGAGCCGGGTGACGATCTTT 1379
 QY 526 LysGlyCysAspThrGlnMetIleTyrAspMetLeuLeuArgLeuLysSerValLeuTyr 545

DB 1380 CAGAACTGTAGGCGCAGCCCTGCTGGAGAGCTGTGTCTGAAGCTGCAGCCCGACCTTAC 1439
 QY 546 LeuProGlyAspPheValCysLysLysGlyGlnIleGlyLysGlnMetCtyrIleIleLys 565
 DB 1440 TCACACAGTGAATATGATATGCCCAAGAGAGATTTGGCCMAAGATGTATCATCATCCGA 1499
 QY 566 HisGlyGlnValGlnValLeuGlyGlyProAspGlyThrLysValLeuValThrLeuLys 585
 DB 1500 GAGGCTCAACTGGCCCTGGT---GCAATGATGGTATTCACACAGTATGCTGTGCTGGT 1556
 QY 586 AlaGlySerValPheGlyGlnIleSerLeuLeuAlaIleGlyIle-----GlyAsn 602
 DB 1557 GCAGGCTCTACTTTGGGAGATCAGATCATCATCAATCAAGAAACATGCTGGGAAC 1616
 QY 603 ArgArgThrAlaAsnValValAlaHisGlyPheAlaAsnLeuLeuThrLeuAspLys 622
 DB 1617 CGCCGACAGCCCAATCAAGACCTTAGGTTATTCAGACCTTATTCCTGAGCCAAAGAG 1676
 QY 623 ThrLeuGlnLysLeuValHisTyrProAspSerGlnArgIleLeuMetLysValAla 642
 DB 1677 GACCTCGGAGGTGCTGAGCGATATCCAAAGACAGACCATCATGAGAGAAAGCA 1736
 QY 643 Arg---ValLeuLeuLys-----GlnLysAlaLysThrAla 653
 DB 1737 CGTGAATCTCTGTAATAATGAACAAGTTGGAGCTGAATGCTGAGGACGCTGATGCC 1796
 QY 654 -----GlnAlaThrProArgLysAspLeuAlaLeuLeuPheProLysGln 671
 DB 1797 CTCAGAGAGCCACAGATCCCG-----CTACGAGGCTTACAGCAGCTGATGAT 1850
 QY 672 ThrProLysLeuPheLysThrLeuLeuGlyIleGlyIleGlyIleValAlaSerLeuAlaArgLeu 691
 DB 1851 CTACAGACCAAGTTTCTGCTGCTCTGCTGCTGAGCTGAGTCCAGCGCATTAAGATTGCT 1910
 QY 692 LeuLysLeuLysArgGlnGlnAlaIleGlnLysLys-----GlnAsnSerGln 707
 DB 1911 TACCGATTAAGACGGCTGAGGTGCGAGCTCGAGACTCGAGATGGCCATGGCCGAGACCTGGCT 1970
 QY 708 GlyIleGlnGlnGlnGlyLysGlnAsnGlnAspLysGlnLysGlnGlnAspLysGln 727
 DB 1971 GAGCTGATGACACGAGGCTGAGCTGAGAGGGAATCTTCCAAAGATGAAGAG----- 2021
 QY 728 LysGlnAsnGlnAspLysGlyLysGlnAsnGlnAspLysAspLysGlyIleArgGln---Pro 746
 DB 2022 -----GSCAGGCGCAGCCAGAGAGGACCCCGAGCTCCAGAGTACCC 2063
 QY 747 GlnGlnLysProLeuAspArgProGlnLysThrAlaSerProIleAlaValGlnGln 766
 DB 2064 CATCCCCATCCCGAGATTTC-CCACTCTTAAGTAATCCAGAGTTGTAATG-----AG 2116
 QY 767 ProHisSerValArgArgThrValLeuProArgGlyThrSerArgIleSerLeuIle 785
 DB 2117 CTTAACTGCTGCAACTCTGTCTATCTGTCTGCGAGATTCACAGACAGAGCGCAATT 2173

RESULT 8
 US-09-799-451-351
 ; Sequence 351, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungang
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei

/ APPLICANT: Wang, Dunrui
 / APPLICANT: Yang, Yonshong
 / APPLICANT: Wehrman, Tom
 / APPLICANT: Ghosh, Reena
 / APPLICANT: Drmanac, Radoje T
 / TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
 / FILE OF INVENTION: Polypeptides
 / FILE REFERENCE: 803
 / CURRENT APPLICATION NUMBER: US/09/799,451
 / CURRENT FILING DATE: 2001-03-05
 / NUMBER OF SEQ ID NOS: 948
 / SOFTWARE: pc_FL_genes Version 2.0
 / SEQ ID NO 351
 / LENGTH: 2366
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (639)..(2363)
 / US-09-799-451-351

Alignment Scores:

Pred. No.:	2, 2e-64	Length:	2366
Score:	669.00	Matches:	191
Percent Similarity:	46.8%	Conservative:	135
Best Local Similarity:	27.4%	Mismatches:	276
Query Match:	15.8%	Indels:	94
		Gaps:	23

US-09-855-828-1 (1-809) x US-09-799-451-351 (1-2366)

QY 73 LeuSerLysLysAsnSerSerGlyAspLeuThrThrAsnProAspProGlnAsnAla 92
 DB 462 ATCAGTAGTAGGCTGCTGTTGTGTCTTAAGAGCCCAAGACAAGATC--- 518
 QY 93 GluProThrGlyThrValProGlnGlnLysGluMetAspProGlyLysGluGly----- 110
 DB 519 -----ACAGCAGAGCCCAAGCAGAGCCCTTCAGGCGTAGGCACATAGTG 566
 QY 111 ProAsnSerProGlnAsnLysProProAlaAlaProValIleAsnGlnLysAlaAspAla 130
 DB 567 CCCAACTCC---AGAACTCCCTCAACAGCAGAGAGGTGTGACATCTACACCCAGCA 623
 QY 131 GlnLeuHisAsnLeuValLysArgMetArgGlnArgThrAlaLeuLysLysLysLeu 150
 DB 624 CCAGACCAAC-----AGAACCATGAGCCAGGACACC-----AAAGTGAAGACA 665
 QY 151 ValGlnGlyAspLeuSerSerProGlnAlaSerProGlnThrAlaLysProThrAlaVal 170
 DB 666 ACAGAG-----TCCAGTCCC-----CCAGCCCATCCCAAGGCGAGGAATGG 707
 QY 171 ProProValLysGluSerAspAspLysProThrGlnHisLysLysLysLeuLeuTrpPhe 190
 DB 708 CTGCCTGCTCTGGAC-----CCATCTGGGGATTACTAC-----TACTGG--- 746
 QY 191 LysValLysLysMetProLeuThrGlnLysLysLysLysLysLysLysLeuProAsnSerIle 210
 DB 746 ----- 746
 QY 211 AspSerLysThrAspArgLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 230
 DB 747 -----TGGCTAACACATGGCTTTCCAGTCATG 776
 QY 231 TrpAsnCyTrpPheIleProLeuAlaValPheProLysGlnThrAlaAspAsnIle 250
 DB 777 TATAACCTATCATCTCTGTCGACAGAGCTGTTCCCGACTGACAGACGGTTATCTG 836
 QY 251 HisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 270
 DB 837 GTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 893
 QY 271 IleGlnProArgLeuGlnIleValArgGlyAspIleIleValAspSerAsnGlnLeu 290
 DB ----- 290

DB 894 GTGCGCTTCCACACAGGATCTTGGAAACAGGCGATCTGTGTGTGACAGAGGTAGATC 953
 QY 291 ArgLysHisLysArgThrSerThrLysPheGlnLeuAspValAlaSerIleLeuProPhe 310
 DB 954 TCGAGTCCCTAGCTTCCGACCTCGAGATTTCTTTCTGTGACCTGTGCTCTCTATGCTCCACA 1013
 QY 311 AspIleCysLysLeuPhePheGly---PheAsnProMetPheArgAlaAsnArgMetLeu 329
 DB 1014 GATGTGCTAGTACGTGCGCTGCGCCGACACACACACCTGAGGCTGAACCGCTTCTC 1073
 QY 330 LysLysLysPhePheGlnPheAsnHisLysLeuGluSerIleMetAspLysAlaLys 349
 DB 1074 CCGCGCGCCCGCTCTTCCAGAGCCCTTCGACCGACAGAGACCCGACAGCTTACCCAAAT 1133
 QY 350 IleLysArgValIleArgThrThrGlyLysLeuLeuPheIleLeuHisIleAsnAlaCys 369
 DB 1134 GCCTTCCCATTTGCCAAGCTAGTGTATTAATTTTGTGTCATTCATTTGAACAGCTGC 1193
 QY 370 ValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 389
 DB 1194 CTATCTTGTGCTTATCCCGGTACCTGCGGCTTCGCGCTGACGCGATGGGTATCCCGGAC 1253
 QY 390 GluGly-----AsnGlnLysLysLysLysLysLysLysLysLysLysLysLysLys 401
 DB 1254 CCGCGCAGCTGCTTGAAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1313
 QY 402 ValArgThrLeuIleThrIleGlyLysLeuProGlnProGlnThrLeuPheGlnIleVal 421
 DB 1314 ACCGTGATACCTACACAGGTGGCGATACCGCCCGCGCAGCGAGGAAGAAAGTACCTC 1373
 QY 422 PheGlnLeuLeuAsnPhePheSerGlyValPheValPheSerSerLeuIleGlyGlnMet 441
 DB 1374 TTCATGTGGGGAGCTCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1433
 QY 442 ArgAspValIleIle---GlyAlaAlaThrAlaAsnGlnAsnLysPheArgAlaCysMetAsp 460
 DB 1434 AGCTTGCTGATCTACAACTGACACCTGACAGTGGCGCTTTTAC-----CCAGAT 1484
 QY 461 AspThrIleAla-----TyrMetAsnAsnLysSerIleProLysLeuValGlnLysArg 478
 DB 1485 CATGCACGTGGGAAGAAGTACATGAAGTGCAGCAGCTCAACCGCAGCTGAGCGGCGA 1544
 QY 479 ValArgThrTrpLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 498
 DB 1545 GTTATTTGACTGTATCACACCTGCAGATCAACAAAGATGACCAACAGAGGTATCCATC 1604
 QY 499 LeuLysThrLeuProThrThrValGlnLeuAlaLeuAlaIleAspValAsnPheSerIle 518
 DB 1605 TTACAGCACTTGCTGAGCGGCTGCGGCGAGAGTGGCTGTCTGTGACCTGTTCAC 1664
 QY 519 IleSerLysValAspLeuPheLysGlyCysAspThrGlnMetIleLysAspMetLeuLeu 538
 DB 1665 CTGAGCCGGGTGACATCTTTTACAACTGTGAGCGCAGCCTCTGAGAGAGTGTGCTG 1724
 QY 539 ArgLeuLysSerValLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLys 558
 DB 1725 AAGCTGCAGCCCGACAGCTTACTCACAGGTGAATGATGACCGCAAGAGAACATGGGC 1784
 QY 559 LysGlnMetLysIleIleLysHisGlyValGlnValGlnValLysGlyLysProAspLysThr 578
 DB 1785 CAAGAGATGATACATATCCGAGAGGTCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1841
 QY 579 LysValLeuValThrLeuLysAlaGlySerValPheGlnGlnLysSerLeuLeuAla 598
 DB 1842 ACACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1901
 QY 599 GlyGly-----GlyAsnArgArgThrAlaAsnValValAlaHisGlyPheAlaAsn 615
 DB 1902 AAAGGAAACATGTCTGGAAACCGCGCACAGCAATCAACAGGCTTAGTTATTCAGAC 1961
 QY 616 LeuLeuThrLeuAspLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 635
 DB 1962 CTATTTGCTGCTGACAG 2021

Db 174 CGCAATCACTCTATTATCAGCATGCTCTTCTGTCGAGGCGGAGAGAGGTTCTTACT 115
Qy 801 lIeGlVallyeGlubysAlayGln 809
Db 114 ATTGAAGTCAAGAAAAAGGCTTAGCA 88
RESULT 12
US-09-949-016-12816
Sequence 12816, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12816
LENGTH: 99370
TYPE: DNA
ORGANISM: Human
US-09-949-016-12816
Alignment Scores:
Pred. No.: 3.05e-49 Length: 99370
Score: 560.00 Matches: 215
Percent Similarity: 18.7% Conservative: 1
Best Local Similarity: 18.6% Mismatches: 5
Query Match: 13.2% Indels: 936
Gaps: 2
DB: 3
US-09-855-828-1 (1-809) x US-09-949-016-12816 (1-99370)
Qy 589 ValPheGluGluLeuSerLeuLeuAlaAlaGlyGlyValAsnArgThrAlaAsnVal 608
Db 93846 ATTTTCTCTCTTACAGCCTTCTTACGACGAGAGAGAGAAACCGTCGAACCTGCAATGTG 93905
Qy 609 ValAlaHisGlyPheAlaAsnLeuThrLeuAspLysThrLeuGlnGluLeu 628
Db 93906 GTGGCCACAGGGGTTTCCCAATCTTTAACTAGACAAAAGACCTCCAGAAATTCTA 93965
Qy 629 ValHisThrProAspSerGluArgIleLeuMetLysLysAla 642
Db 93966 GTGCATTATCCAGATTCTGAAGAGATCCATGAGAAAGC-CAGGTACAACTTTAAA 94024
Qy 642 ----- 642
Db 94025 CACCATTAGAGATGATGAGAGTGTGTTTACTTTGTAAACTTGAGATAGGAGAACGT 94084
Qy 642 ----- 642
Db 94085 ATTATGATTGTGATAAATTGATCACAAGATATGCTTAATGAACAACTATTAAATGA 94144
Qy 642 ----- 642
Db 94145 GGTAACCATTTGAACCTACACAGGTAGATAAATTGCAAGTTTTTAGTAGATTGGCA 94204
Qy 643 -----ArgValLeuLeuLys 647
Db 94205 GAACCTCACAGAGTACTAAACAGCTTTCTCTTACCAAGAGGCTTTTAAAG 94264
Qy 648 GlnLysAlaLysThrAlaGluAlaThrProProArgLysAspLeuAlaLeuLeuPhePro 667
Db 94265 CAGAAAGGCTTAAGACCGCAGAAAGCAACCCCTCCAAAGAAAAAGATCTCCCTCTTCCCA 94324

Qy 668 ProLysGluGluThrProLysLeuPheLysThrLeuLeuGlyGlyThrGlyLysAlaSer 687
Db 94325 CCGAAAGAGAGACACCCAACTGTTTAAACTCTCTAGAGGACACAGGAAAGCAAGT 94384
Qy 688 LeuAlaArgLeuLeuLysLeuLysArgGluGlnAlaAla 700
Db 94385 CTTGCAAGACTACTCAAAATTGAAGCAGAGCAAGCAGC-TCAGTAAATAAGTGAAGTGA 94443
Qy 700 ----- 700
Db 94444 ATGAGCGCTGTGATGAGAGAGGCCCCAGACTAAGTATATACACAAAGCCCACTCTA 94503
Qy 700 ----- 700
Db 94504 ATTCAATTACAGACTGGGATGATTTGGACTAATCTAATTAATTAATCTTCTTTAT 94563
Qy 700 ----- 700
Db 94564 ATATAGCACAATTATTTAACTGCTGAATTCACATATCATCATTTAACCTTCAC 94623
Qy 700 ----- 700
Db 94624 AGGATGTTATAGATGGCTTTAATATGATGATTTATTAACAGAGTATACCTCATAT 94683
Qy 700 ----- 700
Db 94684 TCATAGATTATTTGCAGATTCTATATTGGTGAATCTACTTAATTAATTTATAGTACT 94743
Qy 700 ----- 700
Db 94744 TAAATCAATACTCATGTGCTTTTGTGTGATTTGTGACAAACAGCAGTGAGGTTG 94803
Qy 700 ----- 700
Db 94804 CAAAAATTAAAGTCTTGATGATCATATTTTACGCTGAGTTTGAAGGAGGACATC 94863
Qy 700 ----- 700
Db 94864 TCCTTTCTTTGTTTACGCTGTGATACTATAAGCAATGACCCCTTGCGCGGTGGTGGCT 94923
Qy 700 ----- 700
Db 94924 CACACCTGTAAATCCAGCACTTTGGAGACCAAGCGCGGATCACAGGCGAGAGAT 94983
Qy 700 ----- 700
Db 94984 CGAGCACTTGTACTTAACACGGTGAACCTGTCTTACTGAATAACACAAAAAATTAGC 95043
Qy 700 ----- 700
Db 95044 CCGGCATGGTGACACACACTGTATGTCAGCTACTTGGAGGCTGAGGCAAGAAATTG 95103
Qy 700 ----- 700
Db 95104 CTTGAATCCGGAGGCAAGGTTGTAGTGGAGCATCAACACTGCACCTGAGCTG 95163
Qy 700 ----- 700
Db 95164 GCGCACAGACATACTGTCTCAAAAAACAAACAAACAAACAAACAAACAA 95223
Qy 700 ----- 700
Db 95224 AGAGTGACACTTTTATGTCATGCTTTCCACATTTTGTGCTTTTGTGATGTGTGATT 95283
Qy 700 ----- 700
Db 95284 TTGCTGCTTAAATATAGCCCCCAAGCATAGTCTGAATATCTGTCTAGTCTCTAAGTG 95343
Qy 700 ----- 700
Db 95344 CAAATGCTGTGATGTGCTTCCAGAGAAATATGTGTGTAGTAACTTCAATTCAGGC 95403
Qy 700 ----- 700

SEQ ID NO 17540
LENGTH: 99370
TYPE: DNA
ORGANISM: Human
US-09-949-016-17540

Alignment Scores:

Pred. No.:	3,05e-49	Length:	99370
Score:	560.00	Matches:	215
Percent Similarity:	18.7%	Conservative:	1
Best Local Similarity:	18.6%	Mismatches:	5
Query Match:	13.2%	Indels:	936
DB:	3	Gaps:	2

US-09-855-828-1 (1-809) x US-09-949-016-17540 (1-99370)

```
QY 589 VALPHEGLYLILSESRLEULEUALAAGLYGLYASNAARGTRHRLAASNAVAL 608
DB 93846 ATTTTCTCTTACAGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCATGTG 93905
QY 609 VALAIAHISGLYPHEALASNLLEUTHRLLEUASPLYSLYETHRLNGLNGLLEU 628
DB 93906 GTGGCCACAGGGGTGGCCATCTTTAACTTAGACAAAAGACCTCCAGAAATTTCTA 93965
QY 629 VALHISLYPROASPSESLUARGILELEUMELYSLYSALA----- 642
DB 93966 GTGCATTATCCAGATTCTGAAGAGATCTCATGAAGAAAGC-CAGGTACACCTTAAAA 94024
QY 642 ----- 642
DB 94025 CACCATTAAGATGATGATGATGTTGTTTACTTTGTAACTCGAGATAGGAGAACCGT 94084
QY 642 ----- 642
DB 94085 ATTATGATTGTATAAACTTGTATCACAGATATGTTAATGAACAATAATATGTA 94144
QY 642 ----- 642
DB 94145 GGTAACCATTAAGAACTACACAGATTAGATAAATTGCAGTTTTTTATAGATTTTGCCA 94204
QY 643 ----- 647
DB 94205 GAACCTCTCACAGATTACCTAAACACAGCTTTCTCTTACCACAGAGTGGCTTTAAAG 94264
QY 648 GINLYSALALYSETHRLAAGLUALATHRPROARGLYSASPLEUALLEULEUPHEPRO 667
DB 94265 CAGAAAGGCTAAGACCGCAGAAACCCCTCCAAAGAAAAGATCTGCTCTCCCTCCCA 94324
QY 668 PROLYSGLUGLUETHRPROLYSLEUPHELYSTHRLLEUGLYGLYTHRGLYLSALASER 687
DB 94325 CCGAAAGAAAGAGACACCCCAAACGTTTAAACTCTCTAGAGGACACAGSAAAAGCAAGT 94384
QY 688 LEUALAARGLEULEULYSLEULYSARGGLUGLINALA----- 700
DB 94385 CTTGCAAGACTACTCTCAATATGAAGCAGAGCAAGCAGC-TCAGTAAATAAGTGAGTGA 94443
QY 700 ----- 700
DB 94444 ATGACGCGCTGTCTANTGAGAGAGGCCCCAGACTAATATACACACAAAGCCCACTTA 94503
QY 700 ----- 700
DB 94504 ATTCCATTTACAGACACTGGGATGATTTGGACTAATCTAATACTAATCTTCTGCTTAT 94563
QY 700 ----- 700
DB 94564 ATATAGACATATTATTAACTGCTGAATCCACATATCATCATTTAAACCTCTCAC 94623
QY 700 ----- 700
DB 94624 AGGATGTTTATAGAGTGCTTTAATATGATGATGATTTATATAACAGAGTATACCTCATAT 94683
QY 700 ----- 700
```

```
DB 94684 TCATAGATTATTTGAGATTCTATATGSGTATCTACTACTATATATTATAGTAAGT 94743
QY 700 ----- 700
DB 94744 TAAATCAATACATCATGTGTCTTTGTGTCTATTTGTGACAAACAGCAGTCAGGGTGG 94803
QY 700 ----- 700
DB 94804 CAAAAATTTAAGTTCCTTGATGCATACATTTTCAGCTGAGTTTGAAAAAAGAGGACATC 94863
QY 700 ----- 700
DB 94864 TCCTTTCTTGTTTCAGCTCTGATACATATAAGAAATGACCTTGGCCGGGTGGGTGGCT 94923
QY 700 ----- 700
DB 94924 CACACCTGTATCCAGACACTTTGGAGAACAAAGCGGCGGATCACAGAGCGAGAGAT 94983
QY 700 ----- 700
DB 94984 CGAGACATTTGACTAATACACGCGTGAACCTGTCTCTACTGAAAAACAAAAAATTAGC 95043
QY 700 ----- 700
DB 95044 CGGGCATGSGTCACACACACTGTAGTCCAGCTACTGGGAGGCTGAGGCAAGAGATTG 95103
QY 700 ----- 700
DB 95104 CTTGAATCGGAGGCAAGGTTGTAGTAGCGCGAGATCACAACTGCATCCAGCCTG 95163
QY 700 ----- 700
DB 95164 GCGGACAGACATATCTGTCTCAAAAAACAAACAAACAAACAAACAAACAAACAA 95223
QY 700 ----- 700
DB 95224 AAGATGACACTTTAGTGCCATGCTTCCACATTTTGTGCTTTTGCATGTGTGATTT 95283
QY 700 ----- 700
DB 95284 TTGCTGCTTAAATATAGCCCCCAAGCATAGTCTGAAATACGTCTAGTCTCTAAGTGC 95343
QY 700 ----- 700
DB 95344 CAAAATGCTGTATGTGCTTCCAGAGAAAATATGTGTGTAGTAACTTCAATTCAGGC 95403
QY 700 ----- 700
DB 95404 ATTACAGTGTGTTGCATGAGTTCAATATATGATCAATATATCTCAAAATTAATCAA 95463
QY 700 ----- 700
DB 95464 TTGATCAATTAATAGTGTATCTTAAACAAAAACACATGAAACAAAGTTATATCAT 95523
QY 700 ----- 700
DB 95524 GACCAATTGACAAAAATATATAGCTTGACCATATATCTCATAGGAACCTAATGCTGT 95583
QY 700 ----- 700
DB 95584 ATTTCTCCAGAACAAATGTTCAAGTACTGTCTAATCTGTGTGTGAAAAATTTATAG 95643
QY 700 ----- 700
DB 95644 AACAAACTACATGATGAATAAAAACTGTATATATACAGACATACATATGATATATAA 95703
QY 700 ----- 700
DB 95704 ATAAATTAACCATTTTATACATTTTCAAAATATTCATTAATTACTATATAGTCAAAATGT 95763
QY 700 ----- 700
```


This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 820 Seconds
(without alignments)
5544.871 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 acgttcaaatcgctgcacaaa.....aagaaaggctaacgacataa 2430

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Licensing First 45 summaries

Database :

- 1: Issued Patents NA:*
- 2: /EMC_Celerra_SIDS3/Ptodata/2/ina/1/COMB.seq:*
- 3: /EMC_Celerra_SIDS3/Ptodata/2/ina/5/COMB.seq:*
- 4: /EMC_Celerra_SIDS3/Ptodata/2/ina/6/COMB.seq:*
- 5: /EMC_Celerra_SIDS3/Ptodata/2/ina/7/COMB.seq:*
- 6: /EMC_Celerra_SIDS3/Ptodata/2/ina/H/COMB.seq:*
- 7: /EMC_Celerra_SIDS3/Ptodata/2/ina/PTUS/COMB.seq:*
- 8: /EMC_Celerra_SIDS3/Ptodata/2/ina/PE/COMB.seq:*
- 9: /EMC_Celerra_SIDS3/Ptodata/2/ina/BE/COMB.seq:*
- 10: /EMC_Celerra_SIDS3/Ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2049.4	84.3	2135	US-09-949-016-1074	Sequence 1074, Ap
2	2035.4	83.8	2139	US-09-949-016-5798	Sequence 5798, Ap
3	330	13.6	99370	US-09-949-016-12816	Sequence 12816, A
4	330	13.6	99370	US-09-949-016-17540	Sequence 17540, A
5	329.6	13.6	601	US-09-949-016-38931	Sequence 38931, A
6	329.6	13.6	601	US-09-949-016-205286	Sequence 205286, A
7	329.6	13.6	601	US-09-949-016-205287	Sequence 205287, A
8	329.6	13.6	601	US-09-949-016-38898	Sequence 38898, A
9	202	8.3	601	US-09-949-016-205176	Sequence 205176, A
10	202	8.3	601	US-09-949-016-5678	Sequence 5678, Ap
11	181.2	7.5	2796	US-09-949-016-17420	Sequence 17420, A
12	169.8	7.0	84571	US-09-949-016-38897	Sequence 38897, A
13	151.4	6.2	601	US-09-949-016-205175	Sequence 205175, A
14	151.4	6.2	601	US-09-949-016-38915	Sequence 38915, A
15	147.6	6.1	601	US-09-949-016-205232	Sequence 205232, A
16	147.6	6.1	601	US-09-949-016-205229	Sequence 205229, A
17	144.6	6.0	601	US-09-949-016-38929	Sequence 38929, A
18	144.6	6.0	601	US-09-949-016-205285	Sequence 205285, A
19	143	5.9	601	US-09-949-016-4344	Sequence 4344, Ap
20	132.8	5.5	3266	US-09-949-016-16086	Sequence 16086, A
21	132.8	5.5	3266	US-09-949-016-38918	Sequence 38918, A
22	102.6	4.2	601	US-09-949-016-205235	Sequence 205235, A
23	102.6	4.2	601	US-09-949-016-38908	Sequence 38908, A

C 24	102.6	4.2	601	US-09-949-016-205235	Sequence 205235, A
C 25	93.8	3.9	7218	US-08-232-463-14	Sequence 14, Ap1
C 26	91.4	3.8	601	US-09-949-016-38908	Sequence 38908, A
C 27	91.4	3.8	601	US-09-949-016-205201	Sequence 205201, A
C 28	87	3.6	996	US-09-270-767-15059	Sequence 15059, A
C 29	85.6	3.5	2223	US-08-257-073-4	Sequence 4, Ap11
C 30	79	3.3	1728	US-09-927-267-3	Sequence 3, Ap11
C 31	79	3.3	2308	US-09-927-267-2	Sequence 2, Ap11
C 32	79	3.3	2366	US-09-799-451-351	Sequence 351, App
C 33	78.8	3.2	929	US-09-671-317-14	Sequence 14, App1
C 34	78	3.2	64309	US-09-949-016-14581	Sequence 14581, A
C 35	73.6	3.0	444	US-09-270-767-11944	Sequence 11944, A
C 36	73.6	3.0	7044	US-09-949-016-14113	Sequence 14113, A
C 37	72.8	3.0	1001	US-09-671-317-439	Sequence 439, App
C 38	72.8	3.0	4316	US-09-880-107-3713	Sequence 3713, App
C 39	72.6	3.0	1282	US-10-002-344A-89	Sequence 89, App1
C 40	71	2.9	601	US-09-949-016-38919	Sequence 38919, A
C 41	71	2.9	601	US-09-949-016-38919	Sequence 38919, A
C 42	70	2.9	88002	US-09-949-002-639	Sequence 639, App
C 43	70	2.9	88002	US-09-949-002-717	Sequence 717, App
C 44	68.2	2.8	3117	US-09-614-221A-275	Sequence 275, App
C 45	67.8	2.8	4167	US-09-973-278-700	Sequence 700, App

ALIGNMENTS

```

RESULT 1
US-09-949-016-1074
; Sequence 1074, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL0001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1074
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1074

Query Match      84.3%; Score 2049.4; DB 3; Length 2135;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

340 CCACAAACAAACCGCTGAGCTCTGTTATTAATGAGTAGTCCGATGCCACTTACAC
1 CCACAAACAAACCGCTGAGCTCTGTTATTAATGAGTAGTCCGATGCCACTTACAC
400 AACCTGTGTAAGAAAGATGCTCAAGACAGCCCTTACAGAAAGTTGGTAGAGGA
61 AACCTGTGTAAGAAAGATGCTCAAGACAGCCCTTACAGAAAGTTGGTAGAGGA
460 GATCTTCTCCACCCGACCCAGCCCAAACTGCAAGCCCAAGCCGCTGATCCACAGTA
121 GATCTTCTCCACCCGACCCAGCCCAAACTGCAAGCCCAAGCCGCTGATCCACAGTA
520 AAAAGAAAGGAGATTAAGCAACAGAACTTACTACAGGCTGTTGGTTCAAGTCAAA
181 AAAAGAAAGGAGATTAAGCAACAGAACTTACTACAGGCTGTTGGTTCAAGTCAAA
580 AAGATGCTTTAAACAGAGTACTTAAAGCAATTAAAGTCAAAAGCATGATTATAC

```

[illegible]

Db	1321	AAGGAGAAATGGCAGAGAAATGTATATCATCAAGATGGAAGAGTCCAAGTCTTGG	1380
QY	1720	GGCCCTGATGCTACTAAAGTTCTGGTTACTCTGTGAAGCTGGTGGTGTGGAGAAATC	1779
Db	1381	GGCCCTGATGCTACTAAAGTTCTGGTTACTCTGTGAAGCTGGTGGTGTGGAGAAATC	1427
QY	1780	AGCCTTCAGACAGAGAGAGAAACCGTCGAATGCGCATGGTGGCCCGCGGGTTT	1839
Db	1428	--CCTTCAGACAGAGAGAGAAACCGTCGAATGCGCATGGTGGCCCGCGGGTTT	1485
QY	1840	GCCATCTTTTAACTCAGACAAAAGACCTCCAGAAATTTCTAGTCATTAATCCAGAT	1899
Db	1486	GCCATCTTTTAACTCAGACAAAAGACCTCCAGAAATTTCTAGTCATTAATCCAGAT	1545
QY	1900	TCTGAAAGGATCCTCATGAAGAAAACGAGATGCTTTTAAAGCAGAGCTTAAGCCGA	1959
Db	1546	TCTGAAAGGATCCTCATGAAGAAAACGAGATGCTTTTAAAGCAGAGCTTAAGCCGA	1605
QY	1960	GAAGCAACCTCCAGAAAAGATCTTGGCTCTCTTCCACCGAAAGAGAGACACC	2019
Db	1606	GAAGCAACCTCCAGAAAAGATCTTGGCTCTCTTCCACCGAAAGAGAGACACC	1665
QY	2020	AAACGTTTTAAATCTCTCTAGAGAGACAGAAAGACAGTCTGCAAGCTACTCAAA	2079
Db	1666	AAACGTTTTAAATCTCTCTAGAGAGACAGAAAGACAGTCTGCAAGCTACTCAAA	1725
QY	2080	TTGAAGGAGAGCAGAGCTCAGAAAGAAATTTCTAGAGAGAGAGAGAAAGGA	2139
Db	1726	TTGAAGGAGAGCAGAGCTCAGAAAGAAATTTCTAGAGAGAGAGAGAAAGGA	1785
QY	2140	AAAGAAATGAGATTAACAAAAAGAAATGAGATTAACAAAAAGAAATGAGATTAAC	2199
Db	1786	AAAGAAATGAGATTAACAAAAAGAAATGAGATTAACAAAAAGAAATGAGATTAAC	1845
QY	2200	GGAAAGAAATGAGATTAAGATTAAGAAAGAGAGCACAAGAGAAAGCACTGGAGAGA	2259
Db	1846	GGAAAGAAATGAGATTAAGATTAAGAAAGAGAGCACAAGAGAAAGCACTGGAGAGA	1905
QY	2260	CCTGAATGTACAGAAATCTTATTCAGTGGAGAGAAACCCCACTAGTTAGAGACA	2319
Db	1906	CCTGAATGTACAGAAATCTTATTCAGTGGAGAGAAACCCCACTAGTTAGAGACA	1965
QY	2320	GTTTTTACCAGAGGAGCTTCGTCAATCACTCATTTACAGATGCTCCTCTGTGTAG	2379
Db	1966	GTTTTTACCAGAGGAGCTTCGTCAATCACTCATTTACAGATGCTCCTCTGTGTAG	2025
QY	2380	GGCGGAGAAAGGTTCTTACTATTGAAGTCAAGAAAGGCTAAGCAATA	2430
Db	2026	GGCGGAGAAAGGTTCTTACTATTGAAGTCAAGAAAGGCTAAGCAATA	2076

```

RESULT 2
US-09-949-016-5798
; Sequence 5798, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01107
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5798
;
; LENGTH: 2139
;
; TYPE: DNA
;

```

ORGANISM: Human
US-09-949-016-5798

Query Match 83.8%; Score 2035.4; DB 3; Length 2139;

Best Local Similarity 99.0%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 1; Indels 19; Gaps 2;

```
QY 340 CCACAAAACAAACCCCTGCAGCTCCTGTTATTAATGAGTATGCGATGCCAGCTCAC 399
Db 1 CCACAAAACAAACCCCTGCAGCTCCTGTTATTAATGAGTATGCGATGCCAGCTCAC 60
QY 400 AACCTGTGAAAAAGATGCGTCAAAAGAACAGCCCTCTACAGAAAAAAGTTGTAGAGGA 459
Db 61 AACCTGTGAAAAAGATGCGTCAAAAGAACAGCCCTCTACAGAAAAAAGTTGTAGAGGA 120
QY 460 GATCTCTCTCACCCCGAAAGCCCAAACTGCAGAAAGCCAGCGCTGTACCAAGTA 519
Db 121 GATCTCTCTCACCCCGAAAGCCCAAACTGCAGAAAGCCAGCGCTGTACCAAGTA 180
QY 520 AAAGAAAGGATGATAGCAACAGAACATTAAGCTGAGGCTGTGGTTCAAAGTCAA 579
Db 181 AAAGAAAGGATGATAGCAACAGAACATTAAGCTGAGGCTGTGGTTCAAAGTCAA 240
QY 580 AAGATGCTTTAAACAGAGTACTTAAAGCGAATTAAACTTCAAACAGCATAGATTCA 639
Db 241 AAGATGCTTTAAACAGAGTACTTAAAGCGAATTAAACTTCAAACAGCATAGATTCA 300
QY 640 ACAGATCGACTTACTCTGTGCTCTTGTGCTTGTGCTGCTGCTGCTTAACTGAACTGC 699
Db 301 ACAGATCGACTTACTCTGTGCTCTTGTGCTTGTGCTGCTGCTTAACTGAACTGC 360
QY 700 TGGTTTATACCACTGCGCTCGTCTTCCATATCAACCGCAGACAACATACACTAGG 759
Db 361 TGGTTTATACCACTGCGCTCGTCTTCCATATCAACCGCAGACAACATACACTAGG 420
QY 760 CTTATTTGCGGACATCATATGTGATATCACTTAACTGATATGCTATTTATCCAGCC 819
Db 421 CTTATTTGCGGACATCATATGTGATATCACTTAACTGATATGCTATTTATCCAGCC 480
QY 820 AGACTCCAGTTTGTAAAGAGAGAGACATATATGTGATCTCAATAGAGCTAAAGAAAC 879
Db 481 AGACTCCAGTTTGTAAAGAGAGAGACATATATGTGATCTCAATAGAGCTAAAGAAAC 540
QY 880 TACAGAGCTTCTCAAAATTTAGTGGATGTCGATCAATATCCATTGATATTTGCG 939
Db 541 TACAGAGCTTCTCAAAATTTAGTGGATGTCGATCAATATATCCATTGATATTTGCG 600
QY 940 TACCTCTTCTTGGGTTTAACTCAATGTTTAGAGCAAAATAGAGTGTAAAGTACCTCA 999
Db 601 TACCTCTTCTTGGGTTTAACTCAATGTTTAGAGCAAAATAGAGTGTAAAGTACCTCA 660
QY 1000 TTTTGTGAATTTATCATCACTTAGAGTCTATATAGCAAAAGCATATATCTACAGAGTT 1059
Db 661 TTTTGTGAATTTATCATCACTTAGAGTCTATATAGCAAAAGCATATATCTACAGAGTT 720
QY 1060 ATTGAACAACCTGATGATGCTGTGTTTATTTGCACTTAATAGCGGTGTTATTAACGG 1119
Db 721 ATTGAACAACCTGATGATGCTGTGTTTATTTGCACTTAATAGCGGTGTTATTAACGG 780
QY 1120 GCTTCAAACTATGAAGAAATTTGGCACTACTAGATGGGTGTATAGTGGGAAGAAACGAG 1179
Db 781 GCTTCAAACTATGAAGAAATTTGGCACTACTAGATGGGTGTATAGTGGGAAGAAACGAG 840
QY 1180 TATCTGAAGATGTTATTTATTTGGGCAAGTTGAACCTTTATATACCATTTGGGCTTCCAGAA 1239
Db 841 TATCTGAAGATGTTATTTATTTGGGCAAGTTGAACCTTTATATACCATTTGGGCTTCCAGAA 900
QY 1240 CCACAAACCTTTATTTGAATGTTTTTGAACCTTGAATTTTTTTTTCGGAGTTTTTGG 1299
Db 901 CCACAAACCTTTATTTGAATGTTTTTGAACCTTGAATTTTTTTTTCGGAGTTTTTGG 960
QY 1300 TTCTCAAGTTTAAATGGTCAGATGAGAGATGTGATTTGAGCAGCTACAGCCCAATCAGAAC 1359
Db 1300 TTCTCAAGTTTAAATGGTCAGATGAGAGATGTGATTTGAGCAGCTACAGCCCAATCAGAAC 1359
```

```
Db 961 TTCTCAAGTTTAAATGGTCAGATGAGAGATGTGATTTGAGCAGCTACAGCCCAATCAGAAC 1020
QY 1360 TACTTCCCGCCTGATGATGATGACACCATTCGCTCATGAAACAAATTAATCCATTCCTAA 1419
Db 1021 TACTTCCCGCCTGATGATGATGACACCATTCGCTCATGAAACAAATTAATCCATTCCTAA 1080
QY 1420 CTTGTGCAAAAAGCGAGTTTCGAGCTTGTATGATATATAGATGGAGCTCTCAAGAAATGCTA 1479
Db 1081 CTTGTGCAAAAAGCGAGTTTCGAGCTTGTATGATATATAGATGGAGCTCTCAAGAAATGCTA 1140
QY 1480 GATGAGTCTGATTTGCTTAAAGCCTTACCACTACGCTGTCAGTAAAGCCCTGCCATTGAT 1539
Db 1141 GATGAGTCTGATTTGCTTAAAGCCTTACCACTACGCTGTCAGTAAAGCCCTGCCATTGAT 1200
QY 1540 GTGAACCTTACAGATATACAGCAAAAGTGCATTTGTTCAAG----GGTTGATACACAGAT 1595
Db 1201 GTGAACCTTACAGATATACAGCAAAAGTGCATTTGTTCAAGGCAAGGTGTGATACACAGAT 1260
QY 1596 GATTTATGACATGTTGCTTAAAGATTAACCGTCTCTATTTTGGCTGGTACTTTGTCTG 1655
Db 1261 GATTTATGACATGTTGCTTAAAGATTAACCGTCTCTATTTTGGCTGGTACTTTGTCTG 1320
QY 1656 CAAAAAGGAGAAATTTGSCAAGAAATGTATATCATCAAGCATGAGAAATGCCAAGTTCT 1715
Db 1321 CAAAAAGGAGAAATTTGSCAAGAAATGTATATCATCAAGCATGAGAAATGCCAAGTTCT 1380
QY 1716 TGGAGGCCCTGATGGTACTTAAAGTTCTGTTATCTGTGAAGCTGGGTGGTCTTTGGAGA 1775
Db 1381 TGGAGGCCCTGATGGTACTTAAAGTTCTGTTATCTGTGAAGCTGGGTGGT----- 1431
QY 1776 AATCAGCCCTTACAGAGAGAGAGAGAAACCGTGAACCTGCAATGTGTTGGCCACAG 1835
Db 1432 -----CTTCTAGAGAGAGAGAGAGAAACCGTGAACCTGCAATGTGTTGGCCACAG 1485
QY 1836 GTTTCGCAATCTTTTAACTTATAGCAAAAGACCCCTCAAGAAATTTAGTCAATTATCC 1895
Db 1486 GTTTCGCAATCTTTTAACTTATAGCAAAAGACCCCTCAAGAAATTTAGTCAATTATCC 1545
QY 1896 AGATTTCTGAAGAGATCCCTCATGAAAGAACCGAGTGCCTTTTAAAGCAGAGGCTTAAGC 1955
Db 1546 AGATTTCTGAAGAGATCCCTCATGAAAGAACCGAGTGCCTTTTAAAGCAGAGGCTTAAGC 1605
QY 1956 CGCAGAACCAACCCCTCCAGAGAAAGATCTTGCCTCTCTCCACGAGAAAGAGAGAC 2015
Db 1606 CGCAGAACCAACCCCTCCAGAGAAAGATCTTGCCTCTCTCCACGAGAAAGAGAGAC 1665
QY 2016 ACCCAAACTGTTTAAACTTCTTGAAGGCAACAGAAAGCAAGCTTTGCAAGACTACT 2075
Db 1666 ACCCAAACTGTTTAAACTTCTTGAAGGCAACAGAAAGCAAGCTTTGCAAGACTACT 1725
QY 2076 CAAATTTGAAGGAGAGCAAGCAAGCTCAGAGAAAGAAATTTCTGAAGAGAGAGAGAGA 2135
Db 1726 CAAATTTGAAGGAGAGCAAGCAAGCTCAGAGAAAGAAATTTCTGAAGAGAGAGAGAGA 1785
QY 2136 AGGAAAAAGAAATGAAGATTAACAAAAAGAAATGAAGTAAACAAAAAGAAATGAAGA 2195
Db 1786 AGGAAAAAGAAATGAAGATTAACAAAAAGAAATGAAGTAAACAAAAAGAAATGAAGA 1845
QY 2196 TAAAGAAAGAAAGAAATGAAGATTAAGAAAGAGAGCCAGAGAGAGACCACTGGA 2255
Db 1846 TAAAGAAAGAAAGAAATGAAGATTAAGAAAGAGAGCCAGAGAGAGACCACTGGA 1905
QY 2256 CAGACCTGAAATGTACAGCAAGTCCATTTGCACTGAGAGAGAAACCCCACTCAGTTAGAA 2315
Db 1906 CAGACCTGAAATGTACAGCAAGTCCATTTGCACTGAGAGAGAAACCCCACTCAGTTAGAA 1965
QY 2316 GACAGTTTACCCAGAGAGGACTTCTCGTCAATCACTCAATTATCAGACATGAGCTCTTCTGC 2375
Db 1966 GACAGTTTACCCAGAGAGGACTTCTCGTCAATCACTCAATTATCAGACATGAGCTCTTCTGC 2025
QY 2376 TGAGGGCGAGAGAGAGGTTCTTACTATTGAAGTCAAGAAAAAGGCTAAGCAATAA 2430
Db 2026 TGAGGGCGAGAGAGAGGTTCTTACTATTGAAGTCAAGAAAAAGGCTAAGCAATAA 2080
```



```

; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-205287

```

Query Match	13.6%;	Score 329.6;	DB 3;	Length 601;
Best Local Similarity	99.7%;	Pred. No. 3.5e-71;		
Matches 329;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2101	AGAGAGAAAGAAAATTCTGAAGGAGAGAGAGAAAGAAAAGAAAATGAAAGATTAACA	2166
Db	464	CAGAGAGAAAGAAAATTCTGAAGGAGAGAGAGAAAGAAAAGAAAATGAAAGATTAACA	405
QY	2161	AAAGAAAATGAAGATTAACAAAAGAAAATGAAGATTAAGCAAAAAGAAAATGAAGATTA	2222
Db	404	AAAGAAAATGAAGATTAACAAAAGAAAATGAAGATTAAGCAAAAAGAAAATGAAGATTA	345
QY	2221	GATAAAGAGAGAGAGACCAAGAGAGAGCACTGAGACAGACTGAATGTACAGCAAGTCT	2286
Db	344	GATAAAGAGAGAGAGACCAAGAGAGAGCACTGAGACAGACTGAATGTACAGCAAGTCT	285
QY	2281	ATTGAGATGAGAGAGAAAGCCCACTCACTTAAAGACAGTTTATCCAGAGGACTCT	2344
Db	284	ATTGAGATGAGAGAGAAAGCCCACTCACTTAAAGAGACAGTTTATCCAGAGGACTCT	225
QY	2341	CGTCATATCATCATATATAGCATGAGCTCCCTTGCTGAGAGGCGGAGAGAGGTTCTTACT	2400
Db	224	CGTCATATCATCATATATAGCATGAGCTCCCTTGCTGAGAGGCGGAGAGAGGTTCTTACT	165
QY	2401	ATTGAAAGTCAAAAGAAAAGGCTTAAGCAATTA	2430
Db	164	ATTGAAAGTCAAAAGAAAAGGCTTAAGCAATTA	135

```

RESULT 9
US-09-949-016-38898/c
; Sequence 38898, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38898
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38898

Query Match      8.3%; Score 202; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 8.6e-40;
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      641 CAGATGACCTCATTCCTCTGCTGCTCTGCTGCTCACTCTTGCTTAATCGAAGTGT 700
Db      202 CAGATGACCTCATTCCTCTGCTGCTCTGCTCTTGCTTGTCACTCTTGCTTAATCGAAGTGT 143

QY      701 GGTTTATACCACTGCGGCTCGTCTTCCCATATCAACCGAGACAACATACACTACTGCG 760
Db      142 GGTTTATACCACTGCGGCTCGTCTTCCCATATCAACCGAGACAACATACACTACTGCG 83

QY      761 TTATTGGGACATCATATGTGATATCATCTTAACTTTATGATATGCTATTATCCAGCCCA 820

```

D_b 82 TTAATGGGACATCAATATGTGAATATCATCTAAGTAAATGATATTTATCCAGCCA 2
Q_y 821 GACTCCAGTTTGTAAGAAGAG 842
D_b 22 GACTCCAGTTTGTAAGAAGAG 1

```

RESULT 10
US-09-949-016-205176/c
; Sequence 205176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205176
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205176

```

```

Query Match Summary:      8.3% ; Score 202; DB 3; Length 601;
Best Local Similarity    100.0%; Pred. No. 8.6e-40;
Matches: 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          641 CAGATGCACTCATCTCCTGTGGCTCTTGCTTGCATCTTCGCCATTAACCTGGAACCTGCT   700
              |||
DB           202 CAGATGCACTCATCTCCGTGGCTCTTGCTTGCATCTTCGCCATTAACCTGGAACCTGCT   143
              |||

QY          701 GGTTATTACCACTGGCGCTTCGCTTCCCATATACAACCGCACAACTACACTGAGC   760
              |||
DB          142 GGTTATTACCACTGGCGCTTCGCTTCCCATATACAACCGCACAACTACACTGAGC   83
              |||

QY          761 TTATTGGCAGCATCATATGTGATATCATCTACCTTTATGATATGCTATTATTCAGCCCA   820
              |||
DB           82  TTATTGGCAGCATCATATGTGATATCATCTACCTTTATGATATGCTATTATTCAGCCCA   23
              |||

QY          821 GACTCCAGTTGTGAAGAGAGG 842
              |||
DB           22  GACTCCAGTTGTGAAGAGAGG 1
              |||

RESULT 11
US-09-949-016-5678
; Sequence 5678, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5678

```

LENGTH: 2796
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-5678

Query Match 7.5%; Score 181.2; DB 3; Length 2796;
 Best Local Similarity 49.8%; Pred. No. 2,2e-34;
 Matches 620; Conservative 0; Mismatches 588; Indels 36; Gaps 5;

QY 740 CAGACACATACACTCTGCTTATTCGCGACATCATATGTGATATCATCTTATG 799
 DB 897 CTGATTAACCTAGAAATATGGCTATTTGGATTAACGATCAGACATAGCTATTTATCG 956
 QY 800 ATATGCTATTTATCCAGCCAGACTCCAGTTTGAAGAGGAGACATATATGTGATT 859
 DB 957 ATATG---TTTGTACAAACAGAGCAAGTTTACCTAGAACAAAGACCTGCTGTAAGGAAG 1013
 QY 860 CAATAGCTTAAGAAACACTACAGACCTTCTACAAAATTTCAATTGATGTGCAATCA 919
 DB 1014 AACTTAACCTCAATTAATATATATATATCCAACTTGCAATTTAACTGATGTTCTGTGAC 1073
 QY 920 TTAATACCATTTGATATTTGCTACCTCTTCTTGGGTTTA---ATCCAATGTTAGACCA 976
 DB 1074 TGTATCAACCTGATTTGCTGATTTTAAGTTAGGGTGAACATACCAAAATTAGATTAA 1133
 QY 977 ATAGATGTTAAAGTACACTCTCATTTTGAATTTATCATCATAGATCTATATAG 1036
 DB 1134 ACAGGTTGTACGGTCTCTCGATATGTGAGTTCTTCAGAGAACAAACAAAGACAA 1193
 QY 1037 ACAACCATATATCTACAGAGTATTCGAACAACCTGGATCTGCTGTTATCTGCACA 1096
 DB 1194 ACATACCAACATCTTCAGAGATTTCCAACTTGTATATGATATGTCATCATATATCACT 1253
 QY 1097 TTAATCCTGCTGTTTATTAATCTGAGCTTCAAACTATGAAGATTTGCATCTAGATGG 1156
 DB 1254 GGAACTACATGCTGTCTACTCTATTTCTTAAAGCTATTTGATTTGAAATGATACATGGG 1313
 QY 1157 TGA-----TGATGGGAAGAAACGATATCTGATGTT 1192
 DB 1314 TCTACCTGATATTAATGATCTGAAATTTGGCCGTTTGGCTAATAAATAGTATACAGCC 1373
 QY 1193 ATTATTTGGCAGTTCGAACCTTTAATTAACATTTGTGGCCTTCAGAACCAACAATTTAT 1252
 DB 1374 TTTACTGCTACACCTGACTTGAATTCACATTTGTGTAACACCCCTCCCGTAGGGATT 1433
 QY 1253 TTGAAATGTTTTCACCTCTGATTTTTCGAGATTTTGTGTTCTCCAGTTTAA 1312
 DB 1434 CTGAGTATGCTTTGTGGTGTGATTTCTTAATGGAAGTAAATTTTGTACATCG 1493
 QY 1313 TTGGTCAGATGAGATGATGATGGAAGCACTACACCAATCGAATCTTCCGGCCCT 1372
 DB 1494 TTGGTAACATAGGTCTATGATTTCCAACATGATCGACGACAGACAAATTTCAAGCAA 1553
 QY 1373 GCATGATGACACCATTTGCTACATGAACAATTAATCTTCTAAACTGTGCAAAAGC 1432
 DB 1554 GAATGATGCTATCAAGCAATATATGATTTTGAATGTAAACCAAGATATGGAAGAA 1613
 QY 1433 GAGTTGCACTTGTGATGATATACATGGACCTTCAAGAGATCTAGATAGCTTGATT 1492
 DB 1614 GGGTTTAAATGCTTGTGACTACCTGTGACCAACAAAAACAGTTGATGAGAAAGGAG 1673
 QY 1493 TGGTTAAGCCCTACAGCACTACGCTCAAGTTACCTCCGCACTTGAATGCAATTCAGCA 1552
 DB 1674 TCTTAAAGATATCTACTGATTAACCTAAGACAGAAAAATGCAATCAAGTTCATTTAGACA 1733
 QY 1553 TCATCGACAAAGTGAATGCTGTTCAAGGGTGTGATACACAGATGATTTATGACATGTTGC 1612
 DB 1734 CATTAAGAAAGATAGCATATTTTGTGATGTTGTAAGCTGCTGTTGTGTAAGTTGCTCT 1793
 QY 1613 TAAATGTAATCGCTTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1672
 DB 1794 TGAATTTGGAACCCCAAGCTACAGCTCTGAGATTAATTTTCAAGAAAGGGGATATCG 1853

QY 1673 GCAGGAATATGATATCATCAAGCATGAGAAAGTCCAAAGTCTTGGAGCCCTGATGTGA 1732
 DB 1854 GACGAGAGATGTCATATTAATCAAGAGGCAAACTCCCTGTGTGGCAGATGATGAGTCA 1913
 QY 1733 CTAAAGTTCTGCT---TACTGTGAAGCTGGTCTGCTGTTTGGAGAAATC--AGCCTTC 1786
 DB 1914 CTCAGTTGTGTGATGAGCAGATGCGCAGCTACTCTGCTGATGATCAGCATTTCTTAACATTA 1973
 QY 1787 TAGCAGCAGAGAGAGAAACCTGCAATGTCCTCAATGTGTGTCGCCACGGTTTCCCAATC 1846
 DB 1974 AAGGAGCAAAAGCTGCAATCGAAAGCGCCAAATTTAAAGATTTGGCTACTCAGACC 2033
 QY 1847 TTTTAATCTAGACAAAGAACCCCTCAAGAAATTTAGTGCATTAATCCAGATTTGAAA 1906
 DB 2034 TGTCTGTCTCTCAAAAGATGACCTTATGGAAGCTTTAACTGATGCCAGATGCCAAA 2093
 QY 1907 GGATCTCATGAAGAAAGCCAGAGTCTTTTAAAGCAGAGGCT 1950
 DB 2094 CTATGCTGGAAGAGAAAGGAGCAGATTTTAAATGAAGATGCT 2137

RESULT 12 US-09-949-016-17420

; Sequence 17420; Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VERTEBR, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 17420
 ; LENGTH: 84571
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(84571)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-17420

Query Match 7.0%; Score 169.8; DB 3; Length 84571;
 Best Local Similarity 49.6%; Pred. No. 5.8e-31;
 Matches 571; Conservative 0; Mismatches 547; Indels 33; Gaps 4;

QY 833 TAAGAGGAGAGCAATATGATGATTTCAATAGCTTAAGAAACCTACAGACTTCTA 892
 DB 80762 TAGAACAGAGCTGCTGTGAAGAGAACTTAACTCTAATAATTAATTAATCAACT 80821
 QY 893 CAATTTGAGTTGATGATGCTGATCAATATATACATTTGATATTTGCTACTTCTTGG 952
 DB 80822 TGCATTTTAACTGATATGTTCTGTCACTGATACCACTGATTTTGTGTAAGTTAG 80881
 QY 953 GGTTTA---ATCCAATGTTTAAAGCAAAATAGATGTTAAAGTACATTTCTTTGGAAT 1009
 DB 80882 GGTGAACTATCCAGAAATTAAGTTTAAACAGGTTGTTAAGGTTCTGCTATGTTGAGT 80941
 QY 1010 TTAATCATCACTGATGCTATTAATGAGCAAAAGCATATATCTACAGATTTATGACAA 1069
 DB 80942 TCTTCCAGAGAACAGAAACAGCAAACTATTCACAACTCTTCAGAGATTTCCAACTTG 81001
 QY 1070 CTGAGATCTTGTGTTTATTTCTGCACATTAATGCTGTGTTTAACTGAGCTTCAAACT 1129
 DB 81002 TTAATGATATGTCATCATTTATCTCACTGGAATGCAATGCTGTGTTCTACTCTAATTTCTAAAG 81061

```

OY 1130 ATGAAGATTGGCACTACTAGATGGTGTA-----TGATG 1165
DB 81062 CATTGGATTGGAAATGATGATCGGTCTACCCGATATATATGCTCGAATTTGGCC 81121
OY 1166 GGGAAAGAAACAGATGATCTGAGATGTTATTATTTGGGCACTTGAACCTTTAATTTACATTG 1225
DB 81122 GTTTGGCTAGAAAATAAGTATACAGCCTTTACTGGCTTACACCTGATGCTTGGACTTACCATTTG 81181
OY 1226 GTGGCCCTTCAGAACACAACTTATTGAATGTTTTCACACTGTAATTTTTTTT 1285
DB 81182 GTGAACACACCCCTCCCGTAGAGGATTTGAGATGTTCTTTTGGTGGTTGATTTCTTA 81241
OY 1286 CTGAGTTTTTGTGTTCTCCAGTTTAATTTGTCAGATGAGAGATGATTTGAGAGACGCTA 1345
DB 81242 TTGGAGTGTATTTTGTCTACCATGTTGGTAACTAGTTCTATGATTTCCACATGA 81301
OY 1346 CAGCCATGAAACTACTTCCGCGCTGCATGATGACACCTTGGCTTACATGAAACATT 1405
DB 81302 ATGCAGCCAGACAGAAATTTCAAGCAAGATGATGCTATCAAGCAATATATGCAATTTTC 81361
OY 1406 ACTCCATTCCTAACTGTGTCAGAAAGCGAGTCCGACTGGATGATGAATATATACATGGAGCT 1465
DB 81362 GAAATGTAGCAAAATATATGAAAAGGCTTATTAATGTTTGACTACCTGTGAGCA 81421
OY 1466 CTCAAGAAATGCTAGATGAGTCTGATTGCTTAAGACCCCTACCACTACGCTCCAGTTAG 1525
DB 81422 ACAAATAAACAGTATGAGAAAGAGCTTTAAAGTATCTACCTGATTAACATAAGAGCA 81481
OY 1526 CCCTGCCCTTATGATGAACTTCAGCATATACAGCAAACTGCACTTGTTCAGAGGTTTG 1585
DB 81482 AAATGGCATCAACGTTCACTTACACACTTAAATAAGGATGCGACTTTTGTGATTTG 81541
OY 1586 ATACACAGATGATTTATGATCATGTTGCTTGAAGATTCGTTCTTATTTGGCTGGTG 1645
DB 81542 AAGCTGCTGTGTTGGTGGAGTTGGTCTTAATTTGCAACCCCAAGTCTACAGTCTTGAG 81601
OY 1646 ACTTGTCTGCAAAAAGGAGAAATTTGGCAGAGAAATGATATCATCAAGCATGAGAGAG 1705
DB 81602 ATTATATTGTCAGAAAGGAGGATATCGGACGAGATGATCACTTATCAAGAAAGGCAAC 81661
OY 1706 TCCAGTTCTTTGGAGGCGCTGATGATGATCAAAAGTTCTGTG---TACTGTGAAGCTGGG 1761
DB 81662 TCGCTGTGTGGCAATGATGAGTCACTCACTTGTGTGATTTAGCGGATGTCAGCTACT 81721
OY 1762 TCGTGTGTTGAGAAATC--AGCTTCTAGACAGAGAGAGAAACGTCGAACCTGCCA 1819
DB 81722 TCGGTGATGATGACATTTCTTAATTAAGGAGAGAACTGGCAATGAAAGCGCCA 81781
OY 1820 ATGTGTGCCCCAGGGTTTGCATCTTTTAACCTTACACAAAAGACCTTCCAAAGAA 1879
DB 81782 ATATTAAAGATATTGGCTACTCAGACCTGTCTGTCTCAAAAAGTACCTCATGGAAG 81841
OY 1880 TTCTAGTGTATATCAAGATTTCTGAAAGATCTCTATGAAGAAAGCCAGAGCTTTTAA 1939
DB 81842 CTCTACTGATGATCCAGATGTCAAAACTATGCTGAAAGAAAGGAGAGAGATTTTAA 81901
OY 1940 AGCAGAGAGCT 1950
DB 81902 TGAAGATGCT 81912

```

```

RESULT 13
US-09-949-016-38897/c
; Sequence 38897, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

```

```

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38897
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38897

Query Match
Best Local Similarity 99.3%; Pred. No. 2.4e-27;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 493 GCAAGCCACGGCTGTACCAACAGTAAAGAAAGCGATGATTAAGCCAAAGACATTAC 552
DB 291 GCAAGCCACGGCTGTACCAACAGTAAAGAAAGCGATGATTAAGCCAAAGACATTAC 232
OY 553 TACAGGCTGTGTGTTTAAAGTCAAAAAGATGCTTTAAGAGTACTTAAAGCAATT 612
DB 231 TACAGGCTGTGTGTTTAAAGTCAAAAAGATGCTTTAAGAGTACTTAAAGCAATT 172
OY 613 AAACCTCAACAGCATGATTCAATACAGAT 645
DB 171 AAACCTCAACAGCATGATTCAATACAGAT 139

```

```

RESULT 14
US-09-949-016-205175/c
; Sequence 205175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205175

```

```

Query Match
Best Local Similarity 99.3%; Pred. No. 2.4e-27;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 493 GCAAGCCACGGCTGTACCAACAGTAAAGAAAGCGATGATTAAGCCAAAGACATTAC 552
DB 291 GCAAGCCACGGCTGTACCAACAGTAAAGAAAGCGATGATTAAGCCAAAGACATTAC 232
OY 553 TACAGGCTGTGTGTTTAAAGTCAAAAAGATGCTTTAAGAGTACTTAAAGCAATT 612
DB 231 TACAGGCTGTGTGTTTAAAGTCAAAAAGATGCTTTAAGAGTACTTAAAGCAATT 172
OY 613 AAACCTCAACAGCATGATTCAATACAGAT 645
DB 171 AAACCTCAACAGCATGATTCAATACAGAT 139

```

```

RESULT 15
US-09-949-016-38915/c
; Sequence 38915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38915
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38915
  
```

```

Query Match      6.1%; Score 147.6; DB 3; Length 601;
Best Local Similarity 97.4%; Pred. No. 2,1e-26;
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1336 GGAGCAGCTACAGCCCAATCAGAACTACTTCGGCGCTGCATGATGACACCATTCCTAC 1395
DB      601 GGAGCAGCTACAGCCCAATCAGAACTACTTCGGCGCTGCATGATGACACCATTCCTAC 542

QY      1396 ATGAACAATTACTCCATTCCTTAACCTTGCCAAAGGAGTTGGACTTGGTATGAATAT 1455
DB      541 ATGAACAATTACTCCATTCCTTAACCTTGCCAAAGGAGTTGGACTTGGTATGAATAT 482

QY      1456 ACATGGAGCTCTCAAGAAATGCTAGATGAGTCTG 1489
DB      481 ACATGGAGCTCTCAAGAAATGCTAGATGAGTCTG 448
  
```

Search completed: May 19, 2006, 02:11:03
 Job time : 825 secs

This Page Blank (uspto)